

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GAMBER Examiner #: 7675 Date: 8/7/00
 Art Unit: 1644 Phone Number 308-3997 Serial Number _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

9001/1644 MAILBOX
 If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: 09/249011 / CO

Inventors (please provide full names): B. L. Als

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

SEQ + SEQ INTERFERENCE SEARCH

SEQ ID NOS 7 - NA

8 - AA

5 - NA

6 - AA

REQUEST
 IN
 THANK

RECEIVED
 AUG - 7 - 2001
 TECH/CHEM. DIVISION
 (15131)

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Jan NA Sequence (#) 2 STN _____
 Searcher Phone #: 8128 AA Sequence (#) 2 Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: 8/7 Bibliographic _____ Dr. Link _____
 Date Completed: 8/28 Litigation _____ Lexis/Nexis Chap 2 8/7 - 6⁰⁰ - 1068 - 1072
 Searcher Prep & Review Time: _____ Fulltext _____ Sequence Systems MB1 8/15 - 6⁰⁰ - 1055 - 1063
 Clerical Prep Time: 15 Patent Family _____ WWW/Internet 8/10 - 6⁰⁰ - 1053 - 1057
 Online Time: 20 Other _____ Other (specify) 8/11 - 6⁰⁰ - 1053 - 1057
8/14 - 6⁰⁰ - 1053 - 1057
8/15 - 6⁰⁰ - 1053 - 1057
8/16 - 6⁰⁰ - 875 - 882
8/17 - 6⁰⁰ - 856 - 860
8/18 - 6⁰⁰ - 632 - 636
8/19 - 6⁰⁰ - 455 - 463
8/21 - 6⁰⁰ - 292 - 296
8/22 - 6⁰⁰ - 228 - 232

PTO-1590 (1-2000)

8/23 - 6⁰⁰ - 194 - 198
 8/24 - 6⁰⁰ - 171 - 175
 8/26 - 6⁰⁰ - 93 - 97
 8/27 - 6⁰⁰ - 7K

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 05:41:38 ; Search time 838.43 Seconds
(without alignments)
862.090 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405
Sequence: 1 atgggttggaactgtatcat.....ccctgtcacgcgtctctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da1: *
2: gb_da2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pr1: *
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14: gb_sy: *
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16: em_fun: *
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27: em_sts: *
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43: gb_htg6: *

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71: gb_pi23: *
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73: gb_pi25: *
74: gb_pi26: *
75: gb_pi27: *
76: gb_pi28: *
77: gb_pi29: *
78: gb_pi30: *
79: gb_pi31: *
80: gb_pi32: *
81: gb_pi33: *
82: gb_pi34: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272.2	67.2	446	5	108288 Sequence 4
2	272.2	67.2	462	12	S78361
3	251.4	62.1	405	9	HSIGHX11
4	248.2	61.3	433	5	AR024343 Sequence
5	248.2	61.3	433	5	AR045196 Sequence
6	245	60.5	405	5	I31950 Sequence 68
7	245	60.5	405	5	I78562 Sequence 68
8	245	60.5	405	5	I78617 Sequence 68
9	245	60.5	405	9	HSBUD114H
10	245	60.5	405	12	MUSIGHM195
11	243.4	60.1	405	5	E16346
12	243.4	60.1	1773	5	E14571
13	241.8	59.7	414	11	AF062257
14	241.8	59.7	451	12	MUSANTVDJ
15	241.8	59.7	471	12	MUSANTVDJ
16	241.2	59.6	700	12	MUSIGHMO
17	241.2	59.6	700	12	MUSIGHMO
18	240.2	59.3	402	9	HSVHTB6
19	240.2	59.3	406	12	MUSIGHMX
20	240.2	59.3	443	5	I09505 Sequence 3
21	239.2	59.1	466	12	MMIGRF24
22	239	59.0	418	5	E16338
23	239	59.0	418	5	E16335
24	239	59.0	462	9	HUMIGHVAL

108288 Sequence 4
S78361 AHT107 VH r
X65893 H.sapiens m
AR024343 Sequence
AR045196 Sequence
I31950 Sequence 68
I78562 Sequence 68
I78617 Sequence 68
Z46348 Homo sapien
M83098 Mus musculu
E16346 DNA encodin
E14571 Mouse mRNA
AF062257 Homo sapi
M37621 Mouse anti-
M27788 Mouse Ig ac
J00494 Mouse Ig ac
M25465 Mouse Ig re
Z47222 H.sapiens m
M28221 Mouse Ig re
I09505 Sequence 3
X14623 Murine MRL-
E16328 DNA coding
E16335 DNA coding
M18512 Human (feta

25	238.6	58.9	433	5	I31929	Sequence 18
26	238.6	58.9	433	5	I78541	Sequence 18
27	238.6	58.9	433	5	I78596	Sequence 18
28	237.6	58.7	422	5	AR013861	Sequence
29	237.6	58.7	422	5	AR033835	Sequence
30	237.6	58.7	422	5	AR042495	Sequence
31	237.6	58.7	422	5	AR058375	Sequence
32	237.4	58.6	418	5	E16336	DNA coding
33	237.4	58.6	418	5	E16332	DNA coding
34	237.4	58.6	418	5	E16332	DNA coding
35	237.4	58.6	418	5	E16334	DNA coding
36	237.4	58.6	418	5	E16336	DNA coding
37	237	58.5	405	9	HSIGRX37	
38	237	58.5	411	9	HSVHFL10	
39	237	58.5	452	9	HSE51A15	
40	236.8	58.5	409	23	E11590	DNA encodinn
41	236.8	58.5	484	12	MUSIGHA11	
42	236.8	58.5	490	12	MUSIG4C11A	
43	235.8	58.2	418	5	E16330	DNA coding
44	235.8	58.2	418	5	E16333	
45	235.8	58.2	420	11	AF067121	Homo sapi
46	235.6	58.2	417	11	AF062208	Homo sapi

ALIGNMENTS

	RESULT	1	PAT	02-DEC-1996
	LOCUS	108288		
	DEFINITION	Sequence 4 from Patent EP 0380068.		
	ACCESSION	108288		
	VERSION	108288.1		
	KEYWORDS	GI:589000		
	SOURCE	.		
	ORGANISM	Unknown.		
	REFERENCE	Unclassified.		
	AUTHORS	1 (bases 1 to 446)		
	TITLE	Zerler B.D.		
JOURNAL		An expression system for production of chemtic monoclonal antibodies		
FEATURES		Patent: EP 0380068-A1 & 01-AUG-1990;		
	source	Location/Qualifiers		
		I..446		
BASE COUNT		/organism="unknown"		
ORIGIN		117 a 110 c 113 g 106 t		

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Db	45	ATGGGCTGGAGCTGTATCATCTCTTTCTTGCGAGCAACAGCTTCAGAGTGTGACCTCCAG	104	
QY	61	gtccagctggtgcagttctggtgcttgaaagccttggaagctcagttgaagtgctcc	120	
Db	105	GTCCAGCTGCACACACTCTGGGCTGTAGGCTGTGAGGCTCTGGGGCTTCAGTGAAGATTTC	164	
QY	121	tgcgaagcttcgcggtactacaatcactcagtttatgtcctatcatcagttggtgtgaaagctcct	180	
Db	165	TGCAAGGGGTTCGGGTACACATTCACTGTATTATGCTTCACACTCGGGGTGAAGCGAGTTCAT	224	
QY	181	ggacagggcctcagatgagttcgagttatataattactatgatatcaaacataaac	240	
Db	225	GCAAAAGACTTGAAGTGGATTGGAAATTATTAGTTCTTAAACAATGGTATATCAACTCAAC	284	
QY	241	cagaagtttaagggcaagggccacaatgactgtagacaagtcgacggacagacgactatg	300	
Db	285	CCGAGGTTTAAAGGCAAGGCCAACATGACTGTGAGAAATCCCTCCACGACAGCCTTATG	344	
QY	301	gaacttaagttctttagagatctgagatcagccgcttattactgtgcaagaagcgagctcg	360	

[illegible]

RESULT	2			
LOCUS	S78361			
DEFINITION	S78361	462 bp	mRNA	ROD 07-MAY-1993
	AHT107 VH region-chimeric mouse/human Mab against the human p55			
	IL-2R heavy chain variable region [mice, mRNA Recombinant Partial			
	462 nt].			
ACCESSION	S78361			
VERSION	S78361.1	GI:243052		
KEYWORDS				
SOURCE	Mus sp.			
ORGANISM	Mus sp.			

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REMARK	FEATURES
1 (bases 1 to 462)	Rose, B., Gillespie, A., Wunderlich, D., Barbosa, J. A., Cahill, K., Dzuiba, J., Shedd, D. and Zerler, B.	A chimeric mouse/human anti-IL-2 receptor antibody with enhanced biological activities	Mol. Immunol. 29 (1), 131-144 (1992)	92114885	Gembak staff at the National Library of Medicine created this entry (NCBI 91bseq 78361) from the original journal article. This sequence comes from F191B.	Location/Qualifiers

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/organism="Mus sp."
/db_xref="taxon:10095"
1|.462
/partial
/gene="AHT107 VH region"
61|.462
/partial
/gene="AHT107 VH region"
/note="chimeric mouse/human MAb against the human p55
IL-2R heavy chain variable region; This sequence comes
from Fig1B"
/codon_start=1
/product="AHT107 VH region"
/protein_id="AAB21040.1"
/db_xref="GI:243053"
/translation="MGWSCIILPLAATATSVHSOVALQSGPEVVRGVSVKISCKGSG
GYFTEDALHWKROSHAKSLEMDYGIISYSNGDTSYNFRFGKATMTWDCSSSTAYMEL
ARLTSESAIYYCCARGSNLEMDYGOGFTIVSS"

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[illegible]

[illegible]

QY	121	tcgaagcttcgcggtgaacattcattctatgtatgtataacagtgtagagagctcct	180
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QY	181	ggacaggccctccgatggtatggaggttatatatcttactgtatatacaactacaac	240
Db	181	ggacaaagcgttgatggtgatggatggatgcatcaccgtggcaattgtnaacaaatatttca	240
QY	241	cagaagtttaaggagcacaagccacaatgactgctgaagaagtcgacagacagaccatata	300
Db	241	cagaagtttccagggcagagtgatcaccatttaccagagacacatccgacagacaccttaccg	300
QY	301	gaacttagttcttcttgagatctcgtagagatacggccgttttacttctgtcgaagcggtcgg	360
Db	301	gagctgacacacgttgatgcatctgaaacacacggcgtgtgttacctgtgacagaggttAACCC	360
QY	361	tatatgactactgggtgcgaaggtacccctgttcacgcttccctca	405
Db	361	ttattgcactactggggccaggaacaccttggtacccgttctctca	405
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LOCUS	AR024343	433 bp	DNA
DEFINITION	Sequence 111 from patent US 5795965.		PAT
ACCESSION	AR024343		
VERSION	AR024343.1	GI:3977637	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 433)		
AUTHORS	Tsuchiya, M., Sato, K., Bendig, M. Margaret, Jones, S. Tarrian and Saidha, J. William.		
TITLE	Reshaped human to human interleukin-6 receptor		
JOURNAL	Patent: US 5795965-A 111 18-AUG-1998;		
FEATURES	Location/Qualifiers		
source	1..433		
	/organism="unknown"		
BASE COUNT	94 a	108 c	128 g
ORIGIN			103 t
Query Match	61.3%;	Score 248.2;	DB 5; Length 433;
Best Local Similarity	75.8%;	Pred. No. 3.6e-68;	
Matches 307; Conservative	0;	Mismatches 98;	Indels 0; Gaps 0;
QY	1	atgggtggaactgtatcatctctcttctgtgttaccacagctacaggtgtgactccag	60
Db	16	atggactgtgacctggaagggtcttcttcttggctggtgacgtccagcagctcaccag	75
QY	61	gtccgcgcgtggtgcagatcggcgctgtgagtgaaagccctggtagctgaagtgtcc	120
Db	76	gtgcagcttgtgcactcttgagactgaggtgaaagagcctggggccctcagtgaaaggtttcc	135
QY	121	tgcaagcttcgcggtacacattcaactgatatgtatgatacagtggtgtagacagctcct	180
Db	136	tgcaagcgttctcgatctactcattctcgtatgtattacatracactgggtcgcgacggcccc	195
QY	181	ggacaggccctccgatggtatggaggttatatatcttactgtatatacaactacaac	240
Db	196	ggacaaagcgttgatggtgatggatggaatttggaccctttcaatggtgtgacttgcgtat	255
QY	241	cagaagtttaaggagcacaagccacaatgactgctgaagaagtcgacagacagaccatata	300
Db	256	cagaagtttcaaggagcagatccaccatttaccgagacacatccgacagacaccttaccg	315
QY	301	gaacttagttcttcttgagatctcgtagagatacggccgttttacttctgtcgaagcggtcgg	360
Db	316	gagctgacacacgttgatgcatctgaaacacacggcgtgtgttacctgtgacagaggggtAAC	375
QY	361	tatatgactactgggtgcgaaggtacccctgttcacgcttccctca	405

Db 376 CGCTTGTACTGGGCGCAGGAACCTGTGCACCGTCTCTCA 420

RESULT 5

LOCUS AR045196 433 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 111 from patent US 5817790.

ACCESSION AR045196

VERSION AR045196.1 GI:5966661

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 433)

AUTHORS Tsuchiya, M., Sato, K., Bendig, M., Margaret, Jones, S., Tarran and Saldanha, J. William.

TITLE Reshaped human antibody to human interleukin-6 receptor

JOURNAL Patent: US 581790-A 111 06-OCT-1998;

FEATURES

source 1..433

BASE COUNT 94 a 108 c 128 g 103 t

ORIGIN

Query Match 61.3%; Score 248.2; DB 5; Length 433;

Best Local Similarity 75.8%; Pred. No. 3.6e-68;

Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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Qy 61 gtccagctgtgcaagctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtc 120

Db 76 GTGCACCTTGTGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 135

Qy 121 tgcgaagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtc 180

Db 136 TGCAGAGCTTCTGGATACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 195

Qy 181 ggacagggcctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtc 240

Db 196 GGACAAAGGCTTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 255

Qy 241 cagaagtttaagggcagggcccaatgactgtgagacaagtcgagagcagcagctatag 300

Db 256 CAGAACTTCAAGGGCGAGCTCACATTTACCTGTAGACACATCCGCGAGCACAGCTTACATG 315

Qy 301 gaactagttcttggagctgagagtaagggcgtttatctggtgcaagagggcgtcg 360

Db 316 GAGCTGAGCAGTCTGAGATCTGAGACAGCGCTGTATTACTGTGCGAGAGGGGTTAAC 375

Qy 361 tatatgactactggtgtcaaggtacacctgtcacacctcctca 405

Db 376 CGTTTGTCTACTGGGCGCAGGAACCTGTGTACCGTCTCTCTCA 420

RESULT 6

LOCUS I31950 405 bp DNA PAT 06-FEB-1997

DEFINITION Sequence 68 from patent US 5585089.

ACCESSION I31950

VERSION I31950.1 GI:1822741

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 405)

AUTHORS Queen, C.L., and Selick, H.E.

TITLE Humanized immunoglobulins

JOURNAL Patent: US 5585089-A 68 17-DEC-1996;

FEATURES

Location/Qualifiers

source 1..405

BASE COUNT 101 a 106 c 105 g 93 t

ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;

Best Local Similarity 75.3%; Pred. No. 3.7e-67;

Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatcttcttcttggttacacacagctacaggtgtgcactccag 60

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Qy 121 tgcgaagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtc 180

Db 121 TGCAGAGCTTCTGGATACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 180

Qy 181 ggacagggcctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtc 240

Db 181 GGAAAGAGCTTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 240

Qy 241 cagaagtttaagggcagggcccaatgactgtgagacaagtcgagagcagcagctatag 300

Db 241 CAGAACTTCAAGGGCGAGCTCACATTTACCTGTAGACACATCCGCGAGCACAGCTTACATG 300

Qy 301 gaactagttcttggagctgagagtaagggcgtttatctggtgcaagagggcgtcg 360

Db 301 GACGTCCGAGCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTG 360

Qy 361 tatatgactactggtgtcaaggtacacctgtcacacctcctca 405

Db 361 GCTATGACTACTGGGCGCAGGAACCTGTGTACCGTCTCTCTCA 405

RESULT 7

LOCUS I78562 405 bp DNA PAT 03-APR-1998

DEFINITION Sequence 68 from patent US 5693761.

ACCESSION I78562

VERSION I78562.1 GI:3014716

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 405)

AUTHORS Queen, C.L., Schneider, W.P., and Selick, H.E.

TITLE Polynucleotides encoding improved humanized immunoglobulins

JOURNAL Patent: US 5693761-A 68 02-DEC-1997;

FEATURES

source 1..405

BASE COUNT 101 a 106 c 105 g 93 t

ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;

Best Local Similarity 75.3%; Pred. No. 3.7e-67;

Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatcttcttcttggttacacacagctacaggtgtgcactccag 60

Db 1 ATGGAGTGGAGCTGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 60

Qy 61 gtccagctgtgcaagctcgtggtggtggtggtggtggtggtggtggtggtggtggtggtc 120

Db 61 GTGCACCTTGTGACAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 120

Qy 121 tgcgaagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtc 180

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Db 121 TGCAGGCTTCGTGATACATCTACTGCTACATCAACATGACCTGGGTGAAGCAGACCAT 180
Oy 181 ggacgggcccgcgagtgatggatgattatattactactagaataatacaactacaac 240
Db 181 ggaaagacccttgatgagatgagatattatttcttaccAAAGGGTGAAGTCTGCTCAAC 240
Oy 241 cagaagtttaaggcacaagcccaatgactgagacaagtcgaagcagcagccatata 300
Db 241 CAGAAGTTCAGAGAGCAAGGCCACATTGACTGTAGACAATTCTCCAGCACAGCCTACATG 300
Oy 301 gaacttaattcttgagatctgagatacagcgcttattactgtgcaagcagcgcttg 360
Db 301 GACGTCGCCAGGCTCACAATCTGAGACCTGTGACGTCCTATTACTGTGCAAGAGGGGCCCC 360
Oy 361 tatatgactactgggtgcaagtgatccctgtcaccgctctccta 405
Db 361 GCTATGACTACTGGGTCAAGGAACCTCAGTACCCTCTCTCA 405

RESULT 8
LOCUS 178617 405 bp DNA PAT 03-APR-1998
DEFINITION Sequence 68 from patent US 5693762.
ACCESSION 178617
VERSION 178617.1 GI:3014771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 405)
AUTHORS Queen,C.L., Co,M.Sung, Schneider,W.P., Landolfi,N.F., Coelinhg,K.L.
TITLE Humanized immunoglobulins
JOURNAL Patent: US 5693762-A 68 02-DEC-1997;
FEATURES
source Location/Qualifiers
BASE COUNT 101 a 106 c 105 g 93 t
ORIGIN

Query Match 60.5%; Score 245; DB 5; Length 405;
Best Local Similarity 75.3%; Pred. No. 3.7e-67;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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RESULT 9
LOCUS HSBUD114H 405 bp mRNA PRI 27-OCT-1994
DEFINITION Homo sapiens mRNA for anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b).
ACCESSION 246348
VERSION 246348
KEYWORDS anti-Sm antibody; diversity region; immunoglobulin heavy chain; joining region; variable region.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS Mahmoudi,M., Edwards,J., Cairns,E. and Bell,D.
TITLE Molecular characterization of natural human anti-Sm autoantibodies
JOURNAL unpublished
REFERENCE 2 (bases 1 to 405)
AUTHORS Mahmoudi,M.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario, Medicine and Microbiology and Immunology, University Hospital Room BRE-12, London, Ontario, Canada, N6A 5A5
FEATURES
source Location/Qualifiers
1..405
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="BUD114"
/tissue.type="human tonsil"
/cell.type="B-cell"
1..57
sig_peptide
1..>405
/codon_start=1
/product="anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b)"
/protein_id="CA86467.1"
/db_xref="GI:560840"
/translation="MDWTWRILFLVNAATGAHSQVLYVQSAEYKPKPSAYKVCCKAS
GYTFGTGMWVROAPGQGLGEMMNMINSQGTVMYADQFQGRVTMTROTSLISTAMEL
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58..351
/gene="hVH1.1"
/note="VH segment"
58..351
/gene="hVH1.1"
352..366
/note="D region/close to DK1 and DM1 germline genes"
367..405
/note="JH4b region"
BASE COUNT 92 a 107 c 128 g 78 t
ORIGIN

Query Match 60.5%; Score 245; DB 9; Length 405;
Best Local Similarity 75.3%; Pred. No. 3.7e-67;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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QY 241 cagaagtttaaggagcaagccacatgactgtagacaagtgcagagcagcattatg 300
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Db 241 CAGAAAGTTTCAAGGACAGGACACCATGACAGGACACGCTCCATCAGCAGCCTACATG 300
QY 301 gaacttagtctcttgatcgtgagatacggccgtttattactgtgcaagagcgccctg 360
|||||
Db 301 GAGCTGAGCAGGCTGAGANTGTAGCAGACAGCGCGTGTATGCTGTGAGAGGCTAGAGCT 360
QY 361 tatatgactactggtggttaaggtaacctgtgtaccgctctctca 405
|||||
Db 361 GGATATATACTACTGGGGCCAGGACCTGTGTCACCGTCTCTCA 405

RESULT 10
MUSIGHM195 405 bp mRNA ROD 27-APR-1993
LOCUS Mus musculus Ig heavy chain mRNA V-region, from hybridoma M195.
DEFINITION M83098
ACCESSION M83098.1 GI:195613
VERSION V-region; immunoglobulin; immunoglobulin heavy chain.
KEYWORDS Mus musculus hybridoma M195 cDNA to mRNA.
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Co.M.S., Avdalovic,N.M., Caron,P.C., Avdalovic,M.V.,
AUTHORS Scheinberg,D.A. and Queen,C.
TITLE Chimeric and humanized antibodies with specificity for the CD33
antigen
JOURNAL J. Immunol. 148, 1149-1154 (1992)
MEDLINE 92148135
FEATURES
source Location/Qualifiers
1..405 /organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="hybridoma M195"
/map="chromosome 12"
1..60
sig_peptide /gene="IGH"
/note="putative"
1..405
partial /gene="IGH"
/note="V-region; putative"
/note="V-region: putative"
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AA38370.1"
/db_xref="GI:195614"
/translation="MGMSWIFLFLSGTAVHSEVQLQDSGPGLVKPQASVKISCKAS
GYTFDYNMHMWKQSHGKSLFLEIGYIYPNGGTGYNQKRSATILTVDSSTATMADV
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gene 1..405 /gene="IGH"
mat_peptide 61..405 /gene="IGH"
/note="V-region"
/product="immunoglobulin heavy chain"

BASE COUNT 101 a 106 c 105 g 93 t
ORIGIN

Query Match 60.5%; Score 245; DB 12; Length 405;
Best Local Similarity 75.3%; Pred. No. 3.7e-67;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttctctgtgtacacagctacaggtgtgcaactccag 60
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Db 1 ATGGAGTGAAGCGTGAATCTTCTCTCTCTCTGTGCAAGACTCAGCGCTCCACTCGAG 60
QY 61 gtccagctgtgtcagctctgtgggtcgtgaggtgaagaagcctggagcctcagtgaagtgtcc 120
|||||
Db 61 GTCCAGCTTCAGCAGTCAGACCTGAGCTGTGTAACCTGGGCTTCACAGTGAAGATATCC 120

QY 121 tgcgaagcttcgggtcacatctcagttatgtctatatagctgggtgagagcgctct 180
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Db 121 TGCAGAGCTTCTGGAGTACATTCACACTACAAATGCACTGGGTGAGAGCGCAT 180
QY 181 ggaacagggcctgagtgagtttgagttatcaattacattacatgataataacaactacaac 240
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QY 241 cagaagtttaaggagcaagccacaatgactgtagaagaatgcagagcagcattatg 300
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Db 241 CAGAAATTCAGAGCAAGGACCATGACTGTAGCAAAATTCCTCCAGCACACCTACATG 300
QY 301 gaacttagtctcttgatcgtgagatacggccgtttattactgtgcaagagcgccctg 360
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Db 301 GAGCTCCGACGCTGACATCTGAGGACTGTGAGTCTATGCTGTGCAAGAGGCGCCCC 360
QY 361 tatatgactactggtggttaaggtaacctgtgtaccgctctctca 405
|||||
Db 361 GGTATGACTACTGGGGTCAAGAACTCAGTCACCGTCTCTCA 405

RESULT 11
E16346 405 bp DNA PAT 28-JUL-1999
LOCUS E16346
DEFINITION DNA encoding immunoglobulin VH region of anti-human Fas mouse
monoclonal antibody CH11.
ACCESSION E16346
VERSION E16346.1 GI:5711029
KEYWORDS JP 1998165178-A/9.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Shultz,M. and Watanabe,Y. .
AUTHORS DNA ENCODING VARIABLE REGION OF ANTI-FAS ANTIBODY AND ANTI-PAS
TITLE Patent: JP 1998165178-A 23-JUN-1998;
JOURNAL IGAKU SEIBUTSUGAKU KENKUSHO:KK
COMMENT OS Mus sp. (mouse)
PN JP 1998165178-A/9
PD 23-JUN-1998
PF 01-JUL-1997 JP 1997191769
PR 02-JUL-1996 JP 96P 172228, 09-OCT-1996 JP 96P 268737 PI
SHIBATA MASAO, WATANABE YUKO
PC C12N15/00,C07K16/18,C12P21/02,(C12P21/02,C12N1:91); CC
strandness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..405 /organism="Mus sp."
FT FT /cell_type="hybridoma"
FT FT /cell_line="CH11"
FT sig_peptide 1..57
FT V-region 58..405
FEATURES
source Location/Qualifiers
1..405 /organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 103 a 102 c 102 g 98 t
ORIGIN

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Best Local Similarity 75.1%; Pred. No. 1.2e-66;
Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttctctgtgtacacagctacaggtgtgcaactccag 60
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Db 1 ATGGAGTGAAGCGTGAATCTTCTCTCTCTCTGTGCAAGACTCAGCGCTCCACTCTGAG 60
QY 61 gtccagctgtgtcagctctgtgggtcgtgaggtgaagaagcctggagcctcagtgaagtgtcc 120
|||||

RESULT	12	
E14571		
LOCUS	E14571	
DEFINITION	Mouse mRNA for immunoglobulin heavy chain of anti-human Fas mouse monoclonal antibody CH11.	PAT 28-JUL-1999
ACCESSION	E14571	
VERSION	E14571.1 GI:5709254	
KEYWORDS	CP 1997322796-A.1.	
SOURCE	Mus musculus.	

REFERENCE
AUTHORS
TITLE
DNA CODING VARIABLE REGION OF MONOCLONAL ANTIBODY, AND RECOMBINED

JOURNAL Patent: JP 1997322796-A 16-DEC-1997;
SANKYO CO LTD
OS Mus musculus (mouse)

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FT      /Product='immunoglobulin heavy chain of
anti-human Fas
FT      mouse monoclonal antibody CH11' FT
FT sig-peptide      1. 57
FT V_region      58. 405
FT misc-feature      406. 1770
FT      /Product='constant region'.
      Location/Qualifiers
      1. 1773
      /organism="Mus musculus"
FEATURES
source
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Matches 304; Conservative	0;	Mismatches 101;	Indels 0;	Gaps 0;

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Oy	61	gtccaaagtgtgtgcaagctctggagctgaagctgaagaagccctgaggagctcaagtgaagtgtcc	120
Db	61	GTCGAGCTTCAGCGAGCTGAGGACCTCGAGCTGGTGTGAACCTGGGGGCTTCAGTGAAGATATCC	120
Oy	121	tgcgaagttccggctcacaacttaccgattatgctataaagttgggtggaacagggctccct	180
Db	121	TGCAAGGCTTTGGATGCACACTTACTGACTACACAACATGCACTGGGGGAGCAGAGCCAT	180
Oy	181	ggacagggccctcgagctgagttgagttataattacatcatcagtaataacaaactaac	240
Db	181	GGAAAGAGCCCTGAGTGATGGATTGGAATATATTATTCATTCAATGGTGGTACTGGCTACAC	240
Oy	241	cagaagtttaaggggcacaagccacaaatgactgtatagacaagtcgacagcacaagcctaatg	300
Db	241	CAGAAGTTCAGAGACCAAGGCCACACTTGACTGATTGACAAATTCCTCCACAGCGCTACATG	300
Oy	301	gaacttagttcttggagatctgagatagatgaagggccgtttattactcgtgcagaagcgggctg	360
Db	301	GAGCTCCCGACCCGTGACATCTGAGAGAACTCTGCAATCTATTACTGTGCAAGAAAGTTACTAT	360
Oy	361	tatatgactactcgggttcaagatgaccccttgtaaccgttcccca	405
Db	361	GCATTGCACTATGGGGTCAAGGAACCTCACTACCGCTCTCTCTCA	405

RESULT	13		
LOCUS	AF062257	414 bp	mRNA
DEFINITION	Homo sapiens clone Xu-12 immunoglobulin heavy chain variable region (Jah) mRNA, partial cds.		
ACCESSION	AF062257		
VERSION	AF062257.1	GI:3170980	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		

REFERENCE	1 (bases 1 to 414)
AUTHORS	Wang, X. and Stollar, B. D.
TITLE	Auto-reactivity and Immunoglobulin Vh gene expression in aging humans
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 414)
AUTHORS	Wang, X. and Stollar, B. D.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES	
SOURCE	Location/Qualifiers
	1. .414

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/gene="IGH"
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CDS

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/ gene="IGH"
/ product="immunoglobulin heavy chain variable region"
/ protein_id="A018293.1"
/ db_xref="GI:3170981"
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V_region
58..>414
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BASE COUNT
91 a 111 c 132 g 80 t
ORIGIN

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Best Local Similarity 76.2%; Pred. No. 3.9e-66;
Matches 313; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

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QY 61 gtccagctgtgcaactctgagctgagctgagctgagctgagctgagctgagctgagct 120
Db 61 GTCCAGCTGTGCACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 120
QY 121 tgcgaagcttcgagctacacattacgtatgatacagctgagctgagctgagctgagct 180
Db 121 TGCAGAGCTTCTGATACACCTTCACCGGCTATATGCTGAGCTGAGCTGAGCTGAGCT 180
QY 181 ggacagggcctcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240
Db 181 GGACAGGCTTCTGATACACCTTCACCGGCTATATGCTGAGCTGAGCTGAGCTGAGCT 240
QY 241 cagaagtttaaggcacaagcacaatgactgacagctgagctgagctgagctgagctgagct 300
Db 241 CAGAAGTTTACGGGCAAGGTTACCATGACAGGACAGCTGATACAGGACGCTACATG 300
QY 301 gaactgttcttggagctgagctgagctgagctgagctgagctgagctgagctgagct 359
Db 301 GAGCTGAGCAAGGCTGAGATCTGAGACAGCGCGTGTATTACTGTGAGGACAGCGGA 360
QY 360 -----gtaatagagctgagctgagctgagctgagctgagctgagctgagctgagct 405
Db 361 GCTGCTATTATTGACTGAGGCGGAGGAGCCTGTGCTGCTCTCA 411

RESULT 14
MUSANTVDJ 451 bp DNA ROD 29-OCT-1994
LOCUS MUSANTVDJ
DEFINITION Mouse anti-DNA autoantibody variable region, diversity region, and joining region.
ACCESSION M37621.1 GI:293302
VERSION M37621
KEYWORDS D-region; J-region; V-region; anti-DNA autoantibody.
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Kofler, R., Noonan, D.J., Levy, D.E., Wilson, M.C., Moller, N.P.,
Dixon, F.J., and Theofilopoulos, A.N.
Genetic elements used for a murine lupus anti-DNA autoantibody are
closely related to those for antibodies to exogenous antigens
J. Exp. Med. 161 (4), 805-815 (1985)
JOURNAL MEDLINE
85159423
FEATURES
source
1..451
location/Qualifiers
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"

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103..397
D_segment
398..406
J_segment
407..451
BASE COUNT
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ORIGIN

Query Match 59.7% Score 241.8; DB 12; Length 451;
Best Local Similarity 74.8%; Pred. No. 3.9e-66;
Matches 303; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 1 atgaggttggaactgtatcatcttcttctgttaccacagctacaggtgtgacctccag 60
Db 47 ATGGATGGAGCTGTATCATCTCTTTTGTGAGCAGACACTACAGTGTCCACTCCAG 106
QY 61 gtccagctgtgcaactctgagctgagctgagctgagctgagctgagctgagctgagct 120
Db 107 GTCCAGCTGTGCACTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 166
QY 121 tgcgaagcttcgagctacacattacgtatgatacagctgagctgagctgagctgagct 180
Db 167 TGCAGAGCTTCTGATACACCTTCACCGGCTATATGCTGAGCTGAGCTGAGCTGAGCT 226
QY 181 ggacagggcctcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240
Db 227 GGACAGGCTTCTGATACACCTTCACCGGCTATATGCTGAGCTGAGCTGAGCTGAGCT 286
QY 241 cagaagtttaaggcacaagcacaatgactgacagctgagctgagctgagctgagctgagct 300
Db 287 GAGAAGTTTCAAGGACAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 346
QY 301 gaactgttcttggagctgagctgagctgagctgagctgagctgagctgagctgagct 360
Db 347 CAGCTGAGCAAGCTGAGATCTGAGACTGTGCGTGTATTATTGTGCAAGATTGTGAGCA 406
QY 361 tataagactacagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 405
Db 407 GGGTTTCTTACTGAGGCGCAAGGAGCTGTGCTGCTCTCTCA 451

RESULT 15
MUSIGHPG 471 bp mRNA ROD 27-APR-1993
LOCUS MUSIGHPG
DEFINITION Mouse Ig active mu-chain mRNA V-D-J2-C region, clone 18C10.
ACCESSION M27788.1 GI:195851
VERSION M27788
KEYWORDS C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
SOURCE Immunoglobulin mu-chain; processed gene.
ORGANISM Mouse spleen, cDNA to mRNA, clone 18C10.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 471)
Kaartinen, M., Rocca-Serra, J., and Maekela, O.
Combinatorial association of V genes: One V-H gene codes for three
non-cross-reactive monoclonal antibodies each specific for a
different antigen (phoxalone, NP or GAT)
Mol. Immunol. 25, 859-865 (1988)
JOURNAL MEDLINE
89096973
FEATURES
source
1..471
location/Qualifiers
/organism="Mus musculus"
/ db_xref="taxon:10090"
/ db_xref="GI:195852"
/ protein_id="AA38441.1"
/ note="Ig mu-chain signal peptide"
491..>471
/ note="Ig mu-chain V-D-J2-C region precursor"

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sig_peptide
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/ note="Ig mu-chain V-D-J2-C region precursor"
/ codon_start=1
/ protein_id="AA38441.1"
/ db_xref="GI:195852"
/ translation="MGWSCIIMFLAATATGVSQVQLQPGALVYPGASVYLSKAS
GYFTSYMHVWVQAPGQGLFNGMIGWIPYAKRFQGRVTMTSDISYAVMEL
SRLRSDTAVYCAFTAGAAVFPYWGQGLTVYVSG"

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OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 05:31:28 ; Search time 864.98 Seconds
(without alignments)
2064.765 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405

Sequence: 1 atgggttggaactgatacat.....ccctgtcacgcgtccctca 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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112: em_gss11:*
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114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

117: gb-gss13:*
118: gb-gss14:*
119: gb-gss15:*
120: gb-gss16:*
121: gb-gss17:*
122: gb-gss18:*
123: gb-gss19:*
124: em-gss13:*

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2	224	55.3	417	72	AM408371 UI-HF-BKO
3	220.8	54.5	488	44	A1791363 oh6a09.y
4	220	54.3	513	72	AM402081 UI-HF-BKO
5	219.8	54.3	516	72	AM402422 UI-HF-BKO
6	218.8	54.0	477	72	AM408484 UI-HF-BKO
7	218.2	53.9	587	72	AM403728 UI-HF-BKO
8	215.6	53.2	498	72	AM403806 UI-HF-BKO
9	215.2	53.1	450	72	AM402294 UI-HF-BKO
10	215	53.1	449	72	AM402364 UI-HF-BKO
11	214.4	52.9	427	72	AM402139 UI-HF-BKO
12	213	52.6	485	72	AM403940 UI-HF-BKO
13	212.6	52.5	438	79	AM630198 ui-hf-bko
14	212.4	52.4	517	72	AM408270 UI-HF-BKO
15	211.8	52.3	542	72	AM405977 UI-HF-BKO
16	211.6	52.2	419	72	AM402189 UI-HF-BKO
17	208.2	51.4	448	72	AM402665 UI-HF-BKO
18	207.6	51.3	387	28	AA569186 nm30d10.s
19	207.6	51.3	501	72	AM402603 UI-HF-BKO
20	207.2	51.2	466	72	AM403202 UI-HF-BKO
21	206	50.9	460	72	AM406939 UI-HF-BKO
22	205.6	50.8	508	72	AM403684 UI-HF-BKO
23	204.6	50.5	457	72	AM405627 UI-HF-BKO
24	201.8	49.8	371	72	AM403410 UI-HF-BKO
25	201.4	49.7	461	36	A1201426 q873c06.x
26	200.8	49.6	396	72	AM402942 UI-HF-BKO
27	200.2	49.4	391	79	AM630635 hb85e05.y
28	200.2	49.4	474	72	AM405180 UI-HF-BKO
29	199.8	49.3	321	64	AM130201 x129h05.x
30	199	49.1	435	72	AM402541 UI-HF-BKO
31	198.6	49.0	412	72	AM403256 UI-HF-BKO
32	198.6	49.0	453	46	A1923980 wt94d07.x
33	198.4	49.0	429	79	AM630630 hb85d11.y
34	198	48.9	486	102	AA62845 HS-5207.A
35	197.8	48.8	477	72	AM403686 UI-HF-BKO
36	197.6	48.8	400	79	AM630968 hb90a12.y
37	197.2	48.7	331	72	AM407729 UI-HF-BKO
38	195.4	48.2	418	72	AM401468 UI-HF-BKO
39	193.6	47.8	312	72	AM401829 UI-HF-BKO
40	193.6	47.8	416	72	AM402457 UI-HF-BKO
41	192.8	47.6	344	72	AM403535 UI-HF-BKO
42	191.4	47.3	343	72	AM402227 UI-HF-BKO
43	190.8	47.1	356	72	AM405552 UI-HF-BKO
44	190.2	47.0	437	79	AM629597 hb67d01.y
45	188.6	46.6	528	44	A1799757 wc37g12.x

ALIGNMENTS

RESULT 1
LOCUS AM403591 488 bp mRNA
DEFINITION UI-HF-BKO-abg-b-01-0-UI-T1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056184 5', mRNA sequence.

ACCESSION	AM403591	GI:6922577
VERSION	AM403591.1	
KEYWORDS	EST	
SOURCE	human	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 488)	
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/biopr/image/image.html Seq primer: M13 forward.	
FEATURES	Location/Qualifiers	
source	1..488	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:3056184"	
	/clone_lib="NIH-MGC_36"	
	/tissue_type="lymph"	
	/cell_type="germinal center B cells"	
	/cell_line="MGC85"	
	/lab_host="DH10B (LTI)"	
	/note="vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."	
BASE COUNT	111 a 136 c 140 g 101 t	
ORIGIN		
Query Match	56.0%; Score 226.6; DB 72; Length 488;	
Best Local Similarity	73.5%; Pred. No. 1.5e-58;	
Matches	311; Conservative 0; Mismatches 94; Indels 18; Gaps 1;	
1	atgggttggaactatcatctcttcttggttaccacagctacaggtgtaactccag	60
2	acgagctgacactgcagatcctcttgggtgcacgacacacagccacacccacg	61
61	gtccagctggagctcgtcgtggtggtggaagcctggagctcgtggaaggtgcc	120
62	gtccagctgtgacatcgtgggctgagtggaagcctgggctcgtggaaggttcc	121
121	tgcaaatcttcggtacacatcattcatgatacagtggtgagacagctcct	180
122	tgcaagcttctgcgtatcacctctactatgctatgctatgctgctccgacgccc	181
181	ggacagggcctcagtgatgagttatattatctatgataataacataac	240
182	ggacaaagcctgagtgatgagttatattatctatgataataataatattca	241
241	cagaagtttaagggaggaagccacaatgctgtgagcaagtgagagagagcctatg	300
242	cagaagtttcaaggcagagtcacattgcacagagacacatccgacgacgacctacg	301
301	gaacttaattctagatcgaagataagccgttatactgtaagaagcg-----	354
302	gagctgacagcctgagatctgaagacacagcctgctgtttactgacgacgagagat	361
355	-----gctgtatatagtactcgtgggtcaaggtacacctgttcacgctcc	402
362	tactatggttccagaggttcttcttactacgtgagccaggaacccctgctacccgtcc	421

QY 403 tca 405
Db 422 tca 424

RESULT 2
AM408371 417 bp mRNA EST 16-FEB-2000
LOCUS UT-HF-BK0-abk-c-03-0-UT-RI NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056620 5', mRNA sequence.
ACCESSION AM408371
VERSION AM408371.1 GI:6927428
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 417)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 6, 2000 this sequence version replaced gi:6677425.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
Location/Qualifiers
1..417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056620"
/clone_lib="NIH_MGC_36"
/tissue_type="Lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 91 a 106 c 130 g 90 t

Query Match 55.3%; Score 224; DB 72; Length 417;
Best Local Similarity 77.3%; Pred. No. 8.8e-58;
Matches 272; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 1 atgggttggaactatcatcttcttctgttaccacagctacaggtgtgactccag 60
Db 2 ACGAGGTGACCTGAGAGTCTCTTTGGTGGGACAGCTACAGGTCTCCAGTCCCG 61
QY 61 gtccagctgggtgcaatctgggtggtggaagagctgggaagctcagtgaaagtgtcc 120
Db 62 GTCCAGCTGGGTGCACTGGGGCTGAGGGAAGAGCCGTGGTCTCGGTGAAGGTCTCC 121
QY 121 tgcgaagcttcggtacacatctgatactatcaacagtgggtgagacagctcct 180
Db 122 TGCAAGGCTTCGTGAGGACCTTACACAGCTATCTATCAGTGGGTGCGACAGGCCCT 181
QY 181 ggaacaggtcctcgagtgattgagttatataattactatgataataacaactaac 240
Db 182 GGACAAAGGCTTGAAGTGGATGGAGGATCATCTTCTTGTGTAACAGCAAACTACGCA 241

QY 241 cagaagttaaggccaagccacaatgactgtgagcaagtcgacgacagccctatg 300
Db 242 CAGAACTTCCAGGGCAGAGTCACTTACCGCGAGAGTCCAGACGACGCTTACATG 301
QY 301 gaactagttctttagatctgagatacgccgttattactactgtgcaag 352
Db 302 GAGCTGACGAGCCTGAGATCTGAGGACACGCGCGGTATTTACTGTGCGAGAG 353

RESULT 3
AI791363 488 bp mRNA EST 13-DEC-1999
LOCUS oh68a09.y5 NCI CGAP Kid5 Homo sapiens cDNA clone IMAGE:1472152 5',
DEFINITION similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);,
mRNA sequence.
ACCESSION AI791363
VERSION AI791363.1 GI:5339079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 488)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
On Jun 22, 1998 this sequence version replaced gi:3246905.
Other ESTs: oh68a09.y5
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
www-bio.lnl.gov/bbrp/image/image.html

This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: see original entry for original citation
information
This 5' resequenced clone has no previous 5' data to verify this
new read against
Insert length: 1021 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 438.

FEATURES
Location/Qualifiers
1..488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1472152"
/clone_lib="NCI CGAP Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATATGCGCGCCCAATATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldi.

BASE COUNT 130 a 121 c 142 g 94 t 1 others

Query Match 54.5%; Score 220.8; DB 44; Length 488;
Best Local Similarity 76.7%; Pred. No. 8.7e-57;

Query Match	54.3%	Score 220;	DB 72;	Length 513:
Best Local Similarity	76.3%	Pred. No. 1.6e-56;		
Matches 284; Conservative	0;	Mismatches 85;	Indels 3;	Gaps 1.

Qy	34	accacagctcacgagtgtgcactccaggctcagctgtgtcagctctgtggctgtgaag	93
Db	2	ACGAGGGCTACAGGTGTCCAGTCCAGGTCCAGCTCAGCTGTGCAGTCGTGGCGTGAGGTGAAG	61
Qy	94	aagcccttgagagctcaatgaagaagtgtctctgcaaaagcttcgccgtacaccttacctattat	153
Db	62	AAGCCTGGGTTCTCAATGTAAGAAGTGTCTCCGCAAGGCTTTGTGAGGCACCTTAGCAGCTAT	121
Qy	154	gctatacagttgtgtgagacagcgctccctctgtgacagggccctcgaattgtgatgttaatat	213
Db	122	GCTATTACACTGGGTGCCAGCACAGCCCCCTGTGACAAGGCGCTGTAGTGGATGGAAAGTATCATG	181
Qy	214	attactatgataataacaataacaaccaagaatttaaaggccaagycacaatgactgta	273
Db	182	CCTATCTTGTATTAACAGCAAGCTAACCCACAGAAAGTTCCAGGCGACAGTACAGATTACC	241
Qy	274	gacaagctgcagagacacagcgcctcatatgtaacttgtcttttgagatctgcagatagcgc	333
Db	242	CACCAATCCAGACACACAGCCTACATGAGTGTGACACACCTGTAGATCTGAGGACACAGGCG	301
Qy	334	gttatctaactgtgcaagagcgagcctgtgatatatgtaactactgtgtgcgaagtacacctgtc	393
Db	302	GTGATTACTGTCTCGAGAGAGAGGGGAGTGGCGTG---TCTGGGCGCCAGAGAAACCTGGTTC	358
Qy	394	acagctctcctca	405
Db	359	ACCGTCTCCTCA	370

RESULT	5			
LOCUS	AM402422	516 bp	mRNA	EST
DEFINITION	UI-HF-BKO-aan-c-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054335 5', mRNA sequence.			16-FEB-2000
ACCESSION	AM402422			
VERSION	AM402422.1	GI:6921108		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 516)			
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	On Sep 10, 1999 this sequence version replaced gi:5865948. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www-bio.lnl.gov/bbrp/image/image.html Seq primer: M13 Forward			

FEATURES	
SOURCE	Location/Organisms
	1..516
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:3054335"
	/clone_1ib="NIH_MGC_36"
	/tissue_type="lymph"
	/cell_type="germinal center B cells"
	/cell_line="MGCB5"

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/lab_host="DHI10B (LRT)"
/notes="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      112 a      146 c      157 g      101 t
ORIGIN

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Query Match	54.3%	Score 219.8	DB 72	length 516
Best Local Similarity	76.6%	Pred. No. 1.8e-56		
Matches 269	Conservative	0	Mismatches 82	Indels 0
				Gaps 0

OY 2 tgggttggaaactgtaacatcttcctttcgtgtaccacagctaacagtgtagcaactccagg 61
 ||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 TGGACTGGAACTGGAGGTTCCCTTGTGCGTCACGACACTACAGGTGTCCAAGTCCAGG 67

62 tccaagctggtgcaagtcgtgggctgaagtgaagaagccctggagctcaagtgaagtgtcc 121
 |||||
 68 tccagctggtcagctgtgggctgagcgaagaagccctgggtccctcagtgaaagcttcc 127
 db

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QY 122 gcaagcttcgcgcacacattcactgattatgctatacagtggtgagaaagctcctg 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 GCAAGGCTTCGAGGACCCCTTCAACAGACTATGCTATCAGCTGGGTGCGGAGGCCCTG 187

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OY 182 gacgggcccgcagcttgattgaattataattactatgatatacaaacactacaacc 241
||||| ||||| ||||| | ||| |||||
Db 188 GACAAGGGCTTGAGTGGATGGAGGAAATCCCTATCCTTGCTTAACAAATCTAACCAAC 247

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Oy 242 agaaatttaaggcgcaagcccaaatgatatgttagcaagtcgacgagcaccagctatatg 3011
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 248 AGAAGTTCAGGCGCAGAGTCAGATTACCGCGGCAAAATCCACGACACAGCCTACATGG 3073

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DY 302 aaactagttcttcttgagaatctgaggataaggccgttatattactgtgcgaag 352
 | | | | | | | | | | | | | |
Db 308 AGCTGAGCAGCCTTGATCTGAGGACACGGCCGTGTATTACTGTGCAGAG 358

RESULT	6
AM408484	
LOCUS	AM408484 477 bp mRNA EST 16-FEB-2000
DEFINITION	U1-Hf-BK0-abm-f-07-0-01.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056796 5', mRNA sequence.	

VERSION	AM408484.1	GI:6927541
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 477)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jan 6, 2000 this sequence version replaced gi:6677358.

Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbfp/image/image.html
 Seq primer: M13 forward.

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FEATURES      Location/Qualifiers
      source      1..477
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3056796"
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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LRI)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
ORIGIN
105 a
132 c 145 g 95 t

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Query Match	54.0%	Score 218.8	DB 72	Length 477
Best Local Similarity	76.6%	Pred. No. 3.5e-56		
Matches 268	Conservative 0	Mismatches 82	Indels 0	Gaps 0

Oy 8 ggaactgtatcatctcttcttggttaccaagctacaggtytgtcactccagtcagc 67
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 GGAACCTGAGGTTCCCTCTTGTGGGTGGCAGCACCTACAGGTGCCAGTCCAGTCCAGTCAGC 67

Qy 68 tgggtcagctcttgggctgtaagtgaaagcccttggagctcagtgtaaggtgtctcttcaag 127

Db 68 TGGTGCAGTCTGGGGCTGAGGTGAAGAACCCCTGGTCTCTCGTGAAGGTCTTCTTGCAGG 127

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Oy      128 cttccgcctacacattcaactgaattatgctataacagtgggtgagacaggcctcctgacagg 187
         ||||| |   ||||| |   ||||| |   ||||| |   ||||| |   ||||| |   ||||| |
Db       128 ctTCTGGAGGCAcCtTCACGAcATGTATTAcACTGGGGCGCAcAGGCCCCtTGACAAG 187
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QY 188 gcctcgagtggaattggaagtatttaataattactatgatatacaaaactacaaccagaagt 247
| | | | | | | | | | | | | | | |
Db 188 ggcttgagtcgatggaggatcatcccttattttgtacacaaactgccacacagaagt 247

OY 248 ttaagygcaagggcccaatgactgtgaacaagtcgacggcacaagcctatatgaaetta 307
 | ||||| | ||||| | ||||| | ||||| | ||||| |
Db 248 TCACGGGCAAGTCAACGATTACACGCAGAACCCACGACACAGCTACTGGAGCTGA 307

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Oy      308  gtcccttgagatctcagagatcgcgccttattactgtcagagcgcgc 357
          |  ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      308  gcacccTGAATCTGAGGACACGGCCGCTGTATTACTGTGGAGAGAGGCC 357

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RESULT 7
AM403728

LOCUS	AM403728	587 bp	mRNA	EST	16-FEB-2000
DEFINITION	U1-HF-BKO-abdh-h-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3056487 5', mRNA sequence.				
ACCESSION	AM403728				
VERSION	AM403728.1	GI:6922750			

SOURCE	ORGANISM
human.	<i>Homo sapiens</i>
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
REFERENCE	1 (bases 1 to 587)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bdrip/image/image.html
Seq primer: M13 Forward.
      location/Qualifiers
source      1. .587

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:305648"
/clone_1p="NH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

```

Query Match	53.98;	Score 218.2;	DB 72;	Length 587;
Best Local Similarity	76.48;	Pred. No. 5.7e-56;		
Matches 268;	Conservative 0;	Mismatches 83;	Indels 0;	Gaps 0;

Oy	1	atgggtttgaacctatcatcatctcttccttggtttacacaaactaaagttgtgcacctcaag	60
Db	52	ATGGACTTGGACTCGAGCATCGCATCTTTCTTGSTGGCAGACAGCAACGGTGGCCACTCCAG	111
Oy	61	gtccagctgtgtgcagctcttgagtcctgaagtcgaagaaccctgtggagctcaagtgaagtgctc	120
Db	112	GTTTAGCTGGGTGCAGCTGTGGAGCTGAGAGGTGAAGAGCCTGGGGCTCTACGTGAAGTCTCC	171
Oy	121	tgcaaagcttcctgcgctacacatacctagatgatgctatacagtggtgtgagacagagctct	180
Db	172	TGCAGAGCTTGTGGTTACCTTTACCTTACCAACATGTGATTCACCTTGGTGGCGACAGGCCCT	231
Oy	181	ggacagaggtcctgcagctgtgattctgaagttatataattactatgatataataacaataaac	240
Db	232	GGACAAGGGCTTGATGGATGGATGGATGATCAACCCCTTACATATGATTAACAACAACTATGCA	291
Oy	241	cagaagtttaagggacaagggccacatactatgtagacaagtcgaagagcacacagctatatg	300
Db	292	CAGAGGCTCCAGGGCAGAGTACCGCTGACACACACATCAGACACAGCAGCCTACATG	351
Oy	301	gaacttagtctcttgagatcttgagatacagggcgcttatactactgtgtcaga	351
Db	352	GAAGTGAAGAGCCCTGAGATCCGACCAACAGGCCCTGTATTACTGTGGGAA	402

RESULT	8
LOCUS	AM403806
DEFINITION	AM403806 510 bp mRNA EST 16-FEB-2000
ACCESSION	U1-HF-BKO-abn-b-12-0-U1.t1 NIH_MGC-36 Homo sapiens CDNA clone IMAGE:3056515 5', mRNA sequence.
VERSION	AM403806
KEYWORDS	AM403806.1 GI:6922851
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 510)
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .
COMMENT	National Institutes of Health, Mammalian gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.

Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares lab
 cDNA Library Arrayed by: M.B. Soares lab
 DNA Sequencing by: M.B. Soares lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LUNL at: www-bio.llnl.gov/bdrr/image/image.html

FEATURES	Seq primer: M13 Forward.
source	Location/Qualifiers
	1. 510
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_image="IMAGE:3056615"
	/clone_id="NH_MGC_36"
	/tissue_type="lymph"
	/cell_type="germinal center B cells"
	/cell_line="MGC85"
	/lab_host="DH10B (LRI)"
	/note="Vector: pUT73-Pac; Site_1: NotI; Site_2: Eco RI;
	Constructed from size fractionated cytoplasmic mRNA
	(0.5-1.5kb). Directionally cloned. Cells provided by Louis
	M. Staudt, Ph.D. Library preparation by Maria de Fatima
	Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT	112 a 140 c 151 g 107 t
ORIGIN	

Query Match	53.2%;	Score 215.6;	DB 72;	Length 510;
Best Local Similarity	71.8%;	Pred. No. 3.4e-55;		
Matches 306;	Conservative	0;	Mismatches 99;	Indels 21;
				Gaps 1;

QY	1	atgggttggaactctatcatctctctctgttaccacacacacaggttgagcactccag	60
Db	28	ATGGACCTGGACCTGGAGGATCCTCTTTTGTGTGGCAGACACGACGATGTCACCTCCAG	87
QY	61	gtccaaagctcgtgtcagactcgtggtctgaagctgaagaagccctggaagctcaagtgaagtgc	120
Db	88	GTCAGAGCTGGTGCAGCTCTGGGGCTGAGAGTGAAGAACCTGGGGCCTCAGTGAAGGTTTCC	147
QY	121	tgcnaagcttcgcgtctacacattcactcgaattatgctatacagatgggtgtgaacagggctcct	180
Db	148	TGCAGAGCTTTGTGATACAGCTTACACGTTATGCTATACATTGGGGTCCAGGCCCC	207
QY	181	ggacagggccctcgaagtgtgattggaagttaataattacatcgtataatacactaac	240
Db	208	GGAGAAAGCGTTGATGGTGGATGGATGGATCAACGCTGGCAATGGTACACAAAATATTC	267
QY	241	cagaagtttaagggcacaagccacacaaatctactgtatagaacaagtcgaagacacagcctatg	300
Db	268	CAGGAGTCCAGGGCAGAGTCAACCATTAACGAGGACACAGGCGGAGCACAGCCTACATG	327
QY	301	gaacttagtctcttgagatctgagatcgaagacggcgcttattactcgtgtcagaagcgccctg	360
Db	328	GAGCTGAGACACCTGAGATCTGAGAGAGAGTGGCTCTGATTATTTGTGCAAGAGGAGGGTAC	387
QY	361	tat-----atgagctactcgggggttaagtagtacccttgcacgctc	399
Db	388	GATTTTGGAGCTGTTATTACGCCCTTTGACTACTGGGGCCACGGGAACCTCGGTACCGGTC	447

RESULT	9			
AM402294				
LOCUS	AM402294	498 bp	mRNA	EST
DEFINITION	UI-HF-BKO-aaf-f-06-0-UI.r1 NIH MGC_36 Homo sapiens CDNA clone			
ACCESSION	AM402294			
VERSION	AM402294.1	GI:6920980		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo. 1 (bases 1 to 498)			
AUTHORS	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			

COMMENT

On Mar 8, 1999 this sequence version replaced g1:4388384.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed By: M.B. Soares Lab
DNA Sequencing By: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNT at:
www.bio.lnl.gov/bbr/image/image.html
Seq primer: M13 forward.

FEATURES

Source

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1. 498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054083"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from site fractionated cytoplasmic mRNA
(0.5-1.5k). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
144 c 148 g 98 t

```

BASE COUNT
ORIGIN

Query Match	53.1%	Score 215.2;	DB 72;	Length 498;
Best Local Similarity	72.9%	Pred. No. 4.5e-55;		
Matches 277; Conservative	0;	Mismatches 103;	Indels 0;	Gaps 0;

OY		1	atggagttggaactgtatacatcttcttcgtgtaccaagaactaaagtgtgcaactccag	60
Db		19	ATGAGCTGGACCTGGAGGATCCTTTTGTGGACAGCACGCCAAGAAGCCATCCCAA	78
OY		61	gtccaagctcgtgcagctctcgagctcgaagtgaagaagccctggagctgaagtgtcc	120
Db		79	GTCAGAGCGGTGCAGTCTGGGGCTTGAGGTGAAGAAGCTGGGGCTTAGTGAAGGTCC	138
OY		121	tgcgaagcttcgcgctctacaattcaactgtathtatgctaatacagtytgtagaacagctcct	180
Db		139	TGCAGAGCTTCTGGATTACACTTCACC GGCTACTATATGCACTGGGTTCGACAGGCCCT	198
OY		181	ggcaaggccccgcggtgatgtgsggttatataatttaccatgtataataacaactaac	240
Db		199	GGACAAGGGCTTGATGGATGGAGGATCAACCTTAACATGTGTTGGCAAAACTATGCA	258
OY		241	cagaagtttaaggacaagcccacatatctgtagaagaatgcagcacagacctaatg	300
Db		259	CAGAAGTTTCAAGGGCAGGGTACCATAACCCAGGACAGTTCATCAGACAGTTTAAATG	318
OY		301	gaacttagttctttgagatcttgagatactgagatacggccgtttattactctgtgcaagcggccctg	360
Db		319	GAGCTGAGCAGGCTGGCATCTGACAGACACGGCCGTGATTATCTGTGGAGAGGAGAAATT	378
OY		361	tatatggaactactcgggtca	380
Db		379	CACATATGATAAAGTGTCA	398

RESULT	10
AW402364	
LOCUS	
DEFINITION	449 bp mRNA EST 16-FEB-2000
ACCESSION	U1-HF-BK0-aal-e-12-o-vr.1 NIH/MCC-36 Homo sapiens cDNA clone
VERSION	IMAGEI:3054071 5', mRNA sequence.
KEYWORDS	AW402364.1 GI:6921050 ;

SOURCE ORGANISM

SOURCE	ORGANISM
human.	Homo sapiens
	Eumetazoa: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
	1 (bases 1 to 449)
REFERENCE	
AUTHORS	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)

COMMENT

On Mar 8, 1999 this sequence version replaced gi:4388466.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Straud, M.D., Ph.D.,
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/obrp/image/image.html
Seq primer: M13 Forward.

FEATURES

④

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1/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054071"
/clone_1b="NH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LRI)"
/note="Vector: pRT3-Pac; site_1: NotI; site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafido, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
ORIGIN
102 a 115 c 140 g 92 t

```

BASE COUNT	102 a	115 c	140 g	92 t
ORIGIN				

Query Match	53.1%	Score 215	DB 72	Length 449
Best Local Similarity	75.8%	Pred. No. 5e-55		
Matches 266	Conservative	0	Mismatches 85	Indels 0
				Gaps 0

Oy	2	tgtgttggaaatgataatctctcttctcgtgttaccaaagctaaagtgctgacatcccaag	61
Db	8	TGGACTGGAACTGGAGGGATCCCTCTTTGGTGGGAGGAGGCACAGGAGCCACACTCCAGG	67
Oy	62	tcccaactgtgtcagtcctcgtatgaggtgaagaagcctctggagctcaagtatgaagtgtcct	121
Db	68	TGCAGCTGTGTCATCTTGGGCGCTAGGTGAAAGAGCCTGGGGCGCTCAGTGAAGGTCTTCT	127
Oy	122	gcaaaagcttccgcgtacacatctacatgatatgtctatcacagtgtgtgtagacagctctcg	181
Db	128	GCAAGGCTTCGTGATACACCTTCAACGGCTACTATATGCACTGGGTGCGACAGGCCCTG	187
Oy	182	gacagagcctcgcagtcgtatgtgagttatctaataattactatgataataacaactacaacc	241
Db	188	GACAAGGCGCTTGAGTGGATGGGATGGATCAACCTAATATGTTGGTGCAACAAGATATGCAC	247
Oy	242	agaagtttaagagcgcaagggcccaatgactgtatagaacaagtgcagagcacagcctatatgg	301
Db	248	AGAAATTTCAGGGGACGGGTCCACACTGACCAAGGGACAGCTGCATCAGACACAGCCTACATGG	307
Oy	302	aacttaagttctttgagatcgtatgagatagtcggcgtttatttactgtgcaaaag	352
Db	308	AGCTTAGGAGGCGCTGAGATCTACGACACGGCCCTGTTTACTGTGCGCAGAG	358

RESULT	11
AM402139	
LOCUS	AM402139 527 bp mRNA EST
DEFINITION	16-FEB-2000
	UT-HF-BK0-aba-e-03-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone

IMAGE:3055588 5', mRNA sequence.
 AM402139
 VERSION AM402139.1 GI:6920825
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 1 (bases 1 to 527)
 Unpublished (1999)
 On Mar 8, 1999 this sequence version replaced gi:438206.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.

FEATURES
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 1..527
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3055588"
 /clone_1lb="NIH_MGC_36"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /lab_host="DH10B (LTI)"
 /note="Vector: p7773-Pac. Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 113 a 155 c 156 g 103 t
 ORIGIN

Query Match 52.9%; Score 214.4; DB 72; Length 527;
 Best Local Similarity 75.6%; Pred. No. 7.9e-55;
 Matches 266; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

1 atgggttggaactgtatcatctcttcttggttaccacagctcaggtgtgacactccag 60
 14 ATGGAGTGGAGCTTGAGGAGTTCCTTGTGGTGAGAGCTACAGTGTGCTCCAG 73
 61 gtccagctgtgtcagctctgtggtgagtggaagcctggtgagctcagtgaaagtctcc 120
 74 GTCCAGCTGTGTGAGTCTGGGGCTGAGGTGAAGAAACCTGGCTCCACAGTGAAGGTCTCC 133
 121 tgcgaagcttcggtcactcattcgtatgtctatcagtgaggtgtgaaagaggtctcc 180
 134 TGCAAGGCTTCTGGAGGACCTTCACAGTATTCATACGCTGGGTGCACAGGCCCT 193
 181 ggaacaggtcctcagtgagtttgagttatataattactatgataatacaactaac 240
 194 GGACAGGCTTCAAGTGGATGGAGATCATCCATATCTTTGGTACAAACCTCCGCA 253
 241 cagaagtttaagggcagaagccacaatgactgtatgacaagtgcagagcagacgtctat 300
 254 CAGAACTTCCAGACAGAGACAGATTAACGCGAGCAAGAAATCCACAGGACGCTACATG 313
 301 gaactagttcttgagatctgagtaagcgcgtttattactgtgcaagag 352
 314 GAGCTAGCAGCCTGGAGTCTGAGACAGGCCCTGTATTACTGTGCGAGAG 365

RESULT 12
 AM403940
 LOCUS
 DEFINITION UT-HF-BKO-abn-h-01-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3056881 5', mRNA sequence.
 AM403940
 VERSION AM403940.1 GI:6922908
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 1 (bases 1 to 485)
 Unpublished (1999)
 On May 7, 1998 this sequence version replaced gi:3119607.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.

FEATURES
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 1..485
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3056881"
 /clone_1lb="NIH_MGC_36"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /lab_host="DH10B (LTI)"
 /note="Vector: p7773-Pac. Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 101 a 135 c 152 g 97 t
 ORIGIN

Query Match 52.6%; Score 213; DB 72; Length 485;
 Best Local Similarity 75.1%; Pred. No. 2.1e-54;
 Matches 283; Conservative 0; Mismatches 85; Indels 9; Gaps 1;

38 cagctacaggtgtgcaactccaggtccagctgtgagctcgtggtgaggtgaaagc 97
 12 CAGCTACAGGTGTGCCAGTCCAGTCCAGCTGAGTGTGAGGTGAGTGAAGAAAC 71
 98 ctggaggtcctcagtgaaaggtgtctcgaagcttcgcggcacaacattcattgtgcta 157
 72 CTGGGCTCCTGGGAAGGCTCTCTGCAAGGCTTCTGGAAGCACCTTCACAGCTTACTA 131
 158 tacagtggttgagacaggtctcttgacagaggtcctcagtgagtttgagttatataat 217
 132 TCAGCTGGGTGCGACAGGCCCTTGACAGAGGCTTGAAGTTCGAGAGGATCATCCCA 191
 218 actatgataatacaactacaacccaagtttaaggcagaagccacaatgactgtatagaca 277
 192 TCTTTGATCAACAAGTATGACAGAAATTCACAGGCGAGATTCACAGATTAACAGGAG 251
 278 agtcagcagcagacagctataggaactagttcttgagatctgagtaagcgcgttt 337
 252 AGCTACAGGACAGAGCTACATGAGATTGACAGCCTGTGATCTGAGACAGGCCGTCT 311
 338 attactgtgcaagag-----cggtgtgtatatagactactgtggttcaagttacc 388

Db 312 ATTACTGCGAGAGAGGGGCTTTGGAGTGGCTTTGACTGAGGGCCAGGAAACC 371
 QY 389 ttgtacacgtctctca 405
 Db 372 TGGTACCGCTCTCTCA 388

RESULT 13
 AM630198 438 bp mRNA EST 31-MAR-2000
 LOCUS h19907.y1 NCI_CGAP.GU1 Homo sapiens cDNA clone IMAGE:2969052 5'
 DEFINITION similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA
 sequence.
 ACCESSION AM630198
 VERSION AM630198.1 GI:7376988
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 438)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Oct 19, 1998 this sequence version replaced gi:2442188.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/html/resources.shtml
 Seg primer: -40RP from Glibco
 High quality sequence stop: 422.

FEATURES
 source
 1..438
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2969052"
 /clone_lib="NCI-CGAP_GU1"
 /tissue_type="2 pooled high-grade transitional cell
 tumors"
 /lab_host="DH10B"
 /note="Organ: genitourinary tract; Vector: PCMV-SpOrf6;
 Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
 Primer: Oligo dt. Library constructed by Life
 Technologies."

BASE COUNT 104 a 121 c 125 g 87 t 1 others
 ORIGIN

Query Match 52.5%; Score 212.6; DB 79; Length 438;
 Best Local Similarity 73.1%; Pred. No. 2.7e-54;
 Matches 272; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atgggttgagactatcatcttcttctgtgtacacagctgagtggtgacccag 60
 Db 44 ATGACTCAGCTGAGAGATCTCTTCTGTGGCAGCAGCAGCAGCAGCCAG 103

QY 61 gtccagctgtgtcagctctgtgggtcgtgaagcctgtgagctcagtgaggtgtcc 120
 Db 104 GTCAGAGCTGTGACAGCTGTGGAGCTGAGGTGAAGAGCCGTGGGCTCAAGTGTCTCC 163

QY 121 tgcacagcttcgggtacacattcattatgtctatacagtggtgtgaagacagctctc 180
 Db 164 TGCAGAGTTTCCGGGTAGCCCTCAGTATTTATTCATGCACTGGGTGAGAGGCTCTCT 223

QY 181 gacacggcctcagtgattgagttatattactatgatatacaactacaac 240
 Db 224 GGAGAGAGGCTTGATGATGGAGTGTGATCTTTGAAGAAGGAGAAACACTCTACGA 283

QY 241 cagaagtttaaggcaagccacaatgactgtagaacagtcgacagacagccattatg 300
 Db 284 CAGAAGTTCACAGCGCAGAGTCCACATGACCCGAGACACATCTACAGACACACTCATAG 343

QY 301 gactagtctcttgaagttcagatagcagccgtttattatctgtgcaagagcgccgg 360
 Db 344 AACTGAGCAGCCTGATATCTGAAGACAGCGCGTATATTACTGTGTAACAGGACTGGG 403

QY 361 tatcagctac 372
 Db 404 GATCGAAGCTTC 415

RESULT 14
 AM408270 517 bp mRNA EST 16-FEB-2000
 LOCUS UI-HF-BK0-abj-b-07-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 DEFINITION IMAGE:3056221 5', mRNA sequence.
 ACCESSION AM408270
 VERSION AM408270.1 GI:6927327
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 517)
 AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jan 6, 2000 this sequence version replaced gi:6677324.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html
 Seg primer: M13 Forward.

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3056221"
 /clone_lib="NIH_MGC_36"
 /tissue_type="1 lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LT1)"
 /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldi, Ph.D. and M. Benito Soares, Ph.D."

BASE COUNT 106 a 156 c 156 g 99 t
 ORIGIN

Query Match 52.4%; Score 212.4; DB 72; Length 517;
 Best Local Similarity 77.2%; Pred. No. 3.2e-54;
 Matches 258; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 19 atctctcttcgtgtacacagctacaggtgtgtcacctccaggtgtcagctgtgtgagctct 78
 Db 10 ATCCTCTTCTGTTGGTGGCAGCAGCCACAGGAGGCCACTCCAGGTGCTGAGTGTCT 69

QY 79 ggggctgaagtgaaagcctggaagctcagtgaaagtgctcgcgaagctccgcgtac 138
 DB 70 ggggctgaagtgaaagcctggaagcctcagtgaaagtgctcgcgaagctccgcgtac 129
 QY 139 acattcagatattatgatacagtgagtgaaagcctcgcgaagctccgcgtac 198
 DB 130 accttcacccggctgactgatacagtgagtgaaagcctcgcgaagctccgcgtac 189
 QY 199 attggagtttattatatttctgatacagtgaaagcctcgcgaagctccgcgtac 258
 DB 190 attggagtttattatatttctgatacagtgaaagcctcgcgaagctccgcgtac 249
 QY 259 gccacaatgactgaaagcagtgaaagcctcgcgaagctccgcgtac 318
 DB 250 gtacacattgacacagtgaaagcctcgcgaagctccgcgtac 309
 QY 319 tctgagagtaggcgcgttatttactgtgcaagag 352
 DB 310 tctgagagtaggcgcgttatttactgtgcaagag 343

RESULT 15
 AM405977 542 bp mRNA EST 16-FEB-2000
 LOCUS UI-HE-B10-acv-a-07-0-UI.r1 NIH_MGC_37 Homo sapiens CDNA clone
 DEFINITION IMAGE:3060372 5', mRNA sequence.
 ACCESSION AM405977
 VERSION AM405977.1 GI:6925034
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 542)
 NIH_MGC http://www.ncbi.nlm.nih.gov/MGC/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jul 8, 1999 this sequence version replaced gi:5422625.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLNL at:
 www-bio.lnl.gov/Dbirp/image/image.html
 Seq primer: M13 Forward.

FEATURES

source

1..542
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3060372"
 /clone_1ib="NIH_MGC_37"
 /tissue_type="lymph"
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 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /note="vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonafide, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 129 a 165 c 152 g 96 t
 ORIGIN

Query Match 52.3%; Score 211.8; DB 72; Length 542;
 *Best Local Similarity 71.5%; Pred. No. 5e-54;
 Matches 298; Conservative 0; Mismatches 107; Indels 12; Gaps 1;

QY 1 atgggttgaaagctatcatcttcttctggttaccacagctcagtgctccag 60
 DB 22 atggactgacacgagagatcccttctggttaccacagctcagtgctccag 81
 QY 61 gtccagctggtgagctcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 120
 DB 82 gtccagctggtgagctcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 141
 QY 121 tgcagagcttcgagctcagctcagctcagctcagctcagctcagctcagctcag 180
 DB 142 tgcagagcttcgagctcagctcagctcagctcagctcagctcagctcagctcag 201
 QY 181 ggaacagagcttcgagctcagctcagctcagctcagctcagctcagctcagctcag 240
 DB 202 ggaacagagcttcgagctcagctcagctcagctcagctcagctcagctcagctcag 261
 QY 241 cagaagtttaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
 DB 262 gagaagttccagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 321
 QY 301 gaacttagtcttctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 360
 DB 322 gacctgagcagccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 381
 QY 361 ta-----tatgactactggtgagtgagtgagtgagtgagtgagtgagtgagtgag 405
 DB 382 aacgagcgcgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 438

Search completed: August 27, 2000, 06:08:49
 Job time: 2241 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 05:53:23 ; Search time 72.06 Seconds

(without alignments)
1406.159 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405

Sequence: 1 atgggttgacgtatcat.....cccttgacgcgtccctca 405

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.2	68.4	524	014802	Encodes murine anti-R5-5-D6 anti-ICAM-Sequence encoding Anti-human Fas hum
2	277.2	68.4	524	014852	Encodes murine anti-R5-5-D6 anti-ICAM-Sequence encoding Anti-human Fas hum
3	272.2	67.2	446	005554	Anti-human Fas hum
4	265.8	65.6	1767	061363	Anti-human Fas hum
5	265.8	65.6	1768	061364	Anti-human Fas hum
6	254.4	62.8	424	042717	Anti-human Fas hum
7	253.6	62.6	451	066702	DREG-200 Humanized Anti-Fas humanised
8	253.6	62.6	2071	070080	Anti-Fas humanised
9	248.8	61.4	457	070104	Anti-Fas humanised
10	248.8	61.4	2077	070079	Anti-Fas humanised
11	245	60.5	405	033947	Anti-CD3 antibody
12	243.4	60.1	405	033764	CDNA encoding a va
13	243.4	60.1	1773	088869	H chain subunit of
14	243.4	60.1	1773	088869	Anti-human Fas mon
15	242.2	59.8	478	088433	EST clone GF196. N
16	241.8	59.7	433	024790	Anti-Tac antibody
17	240.8	59.5	421	073624	CDNA for humanised
18	240.8	59.3	443	091820	DNA sequence of th
19	239	59.0	418	039405	Humanised anti-HM1
20	239	59.0	418	039350	Humanised anti-HM1
21	239	59.0	418	039357	Humanised anti-HM1
22	239	59.0	418	070581	Humanised anti-HM1
23	239	59.0	418	059116	Anti-human HM1.24
24	238.6	58.7	433	005600	Anti-Tac antibody
25	237.6	58.7	422	056413	Anti-Tac heavy cha
26	237.6	58.7	422	054863	Murine ICR-1.1 V-H
27	237.6	58.7	422	069185	Murine antibody IC
28	237.6	58.7	422	021879	DNA encoding antib
29	237.4	58.6	418	039402	Humanised anti-HM1
30	237.4	58.6	418	039402	Humanised anti-HM1
31	237.4	58.6	418	039399	Humanised anti-HM1
32	237.4	58.6	418	039354	Humanised anti-HM1
33	237.4	58.6	418	039356	Humanised anti-HM1

34	237.4	58.6	418	1	V39358	Humanised anti-HM1
35	237.4	58.6	418	1	V39348	Humanised anti-HM1
36	237.4	58.6	418	1	V07562	Anti-human HM1.24
37	237.4	58.6	418	1	V59117	HM1.24 antibody he
38	237	58.5	477	1	012057	Sequence encoding
39	237	58.5	477	1	012013	Sequence encoding
40	236.8	58.5	409	1	094539	Human/murine chime
41	236.8	58.5	409	1	038653	Chimeric human/mu
42	236	58.3	421	1	073633	CDNA for humanised
43	235.8	58.2	418	1	V39396	Humanised anti-HM1
44	235.8	58.2	418	1	V39352	Humanised anti-HM1
45	235.4	58.1	588	1	043385	H-chain V-region o

ALIGNMENTS

RESULT	1	Location/Qualifiers
014802	Standard; DNA; 524 BP.	
ID	014802	
AC	13-FEB-1992 (first entry)	
DT	Encodes murine anti-ICAM monoclonal antibody heavy chain.	
DE	Inter-cellular adhesion molecule; variable region; V(H); mouse;	
KW	R5-5-D6 murine Mab; complementarity determining region; CDR; ds.	
OS	Mus musculus.	
FS	Key	
FT	signal_peptide 34..90	
FT	/*tag- a	
FT	/standard_name= leader	
FT	34..524	
FT	/*tag- b	
PN	WO9116927-A.	
PD	14-NOV-1991.	
PF	29-APR-1991; U02942.	
PR	27-APR-1990; GB-009549.	
PA	(CELL-) CELTECH LTD.	
PA	(BOE) BOEHRINGER INGELHEIM PHA.	
PI	Adair JR, Athwal DS, Rothlein RA.	
DR	WPI: 91-35353/48.	
DR	P-PSDB: R13060.	
PT	New humanised CDR-grafted anti-ICAM antibodies - used to treat	
PT	and prevent inflammation (e.g. psoriasis) tumours, viral	
PS	infections and asthma and in diagnosis	
PS	Disclosure; Fig 2: 83pp; English.	
CC	The heavy chain sequence was isolated from a CDNA library prepd. from	
CC	hybridoma cell line R5-5-D6 which secretes murine IgG2a/Kappa	
CC	antibody. The library was screened using a 980bp BamHI-EcoRI	
CC	fragment of a previously isolated mouse IgG2a constant region	
CC	clone. The murine framework-encoding sequences (i.e. not encoding	
CC	CDRs) will be replaced by human framework sequences to produce	
CC	recombinant (CDR-grafted humanised) antibody molecules having	
CC	specificity for ICAM-1.	
CC	Sequence 524 BP; 128 A; 130 C; 135 G; 131 T;	
SQ		
Query Match	68.4%; Score 277.2; DB 1; Length 524;	
Best Local Similarity	81.4%; Pred. No. 3.1e-71;	
Matches 337; Conservative	0; Mismatches 68; Indels 9; Gaps 1;	
0Y	1 atgggttgacgtatcatctcttcttggttaccacagctacagtggtgacctccag 60	
Db	34 ATGGGTGGACGTATCATCTTCTTGTGTGACACAGCTAAGGTCACATCTCCAG 93	
0Y	61 gtccagctggtgacgtctggtggtggaagagcctggagctcagtgaaagtgtcc 120	
Db	94 GTCCAGCTGACGACGTCTGGGCTGAGCTGTGAGCCCTGGGGCTCAGTGAAGATTCC 153	
0Y	121 tgcgaagcttcggtctacacattcagatattctatacagtggtggagacagctctc 180	
Db	154 TGCAAGGTTCCGGCTACACATTGATTATGCTATACACTGGGTGAAGAGATCAT 213	
0Y	181 ggaagggccctcgagtgatgtgagttataataataataataataataataacac 240	

Query Match	68.4%	Score 277.2	DB 1	Length 524
Best Local Similarity	81.4%	Pred. No. 3.1e-71		
Matches 337	Conservative 0	Mismatches 68	Indels 9	Gaps 1

Query	1. atgggttggaactgtatcatctcttcttggtgtaccacagcctacaggtgtgcaactccag	60
34	atgggttggaactgtatcatctcttcttggtgtaccacagcctacaggtgtgcaactccag	93

OY	61	gtccagctcgtgcagtcttcgggcttgaaggacccgggagctcaatgaagttccc	120
Dd	94	gtccagctgcaccactcttgcccttagcctggctagaacctggcgctctcatgatgaattttcc	153
OY	121	tgcacaagcttccgggttaacatactacactgatctgattctgatacaagttgggtgaaagagctcct	180
Dd	154	tgcAAGGGTTCGGGTACACATTGATTTGATTATGCTATATACACTGGGTGAAGAAGATCAT	213
OY	181	ggacagggccctcgaagttgattggagttattaatatctactatgataatacaactaacac	240
Dd	214	GCAAAAGACTTAAGATGGATTGGAAATTATTAATCGCTTACTCTGGGGACACAACAATCACAC	273
OY	241	cagaagctttaaggaggaagccacaatgactgtagacagctgcagacagacagcttatatg	300
Dd	274	CAGAAGTTTAAGGCGCAGAGCCCAATGCATGCTGTGGACAATCTCCAACACACACTATTGG	333
OY	301	gaacttagtcttccttgagatctgagatacagcgccgtttacttactgycaaagcggcttgg	360
Dd	334	GAACTTGCCAGATTTGACATCTGAGGATTTCTGCCATCTATTACTGTGCAAGAGGGGATAT	393
OY	361	-----tatatgactactcgggggtcaaagttacccttgtcacogtctcccca	405
Dd	394	TTACTACTCTCTCTTGACTACTGAGGGGCCAACACCACACTCTACAGTCCCTCA	447
RESULT	3		
ID	005554		
AC	005554 standard; DNA: 446 BP.		
AD	005554.		
DE	10-DEC-1990 (first entry)		
DR	Sequence encoding variable region of murine AHT 107 heavy chain.		
KM	Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss.		
OS	Mus sp.		
FH	Key	Location/Qualifiers	
FT	cds	45..446	
ET		/*tag= a	
PN	EP-380068-A.		
PD	01-AUG-1990.		
PF	24-JAN-1990; 101351L		
PR	24-JAN-1989; US-301216.		
PK	04-DEC-1989; US-441702.		
PA	(MOLE-) MOLECULAR THERAPU.		
PI	Zerler B;		
DR	WPI; 90-232892/31.		
P	P-PSTD; R06250.		
PT	Expression vectors for producing chimeric monoclonal antibodies -		
PS	which express human constant region and non-human variable region		
PS	Disclosure; P: English.		
CC	MABs comprising mouse CH and CL constant regions with human		
CC	variable regions may be used to create mouse/human hybrid MABs,		
CC	which have a longer serum half-life. Method can be used to produce		
CC	Abs against interleukin-2 receptor and tumour necrosis factor.		
SQ	Sequence 446 BP; 117 A; 110 C; 113 G; 106 T;		
Query Match	67.2%; Score 272.2; DB 1; Length 446;		
Best Local Similarity	81.2%; Pred. No. 8, le-70;		
Matches 329; Conservative	0; Mismatches 73; Indels 3; Gaps		
OY	1	atgggtctggaactgtatacatcttcttcttcgtgttacacagactacagtggtgactccag	60
Dd	45	ATGGGCTGAGAGTGTATCATCTCTTTCTTGGCAGCAACAGTACAAAGTGCACCTCCAG	104
OY	61	gtccagctcgtgtcagatctcggggctgaagtgaagaagcctcggagctcagtgaaagtgtcc	120
Dd	105	GTCCAGCTGCACCACTCTGGGCTTAGGGTGGAGAGCCCTGGGGTCTCACTGAAGAATTTCC	164
OY	121	tgcAagctcgggttacatcatactactgatatgtctatacagttggttgagacagctct	180
Dd	165	TGCAAGGGTTCGGGTACACATTCTGATTTATGCTCTTCACATGGGTGAAGAGACTCAT	224
OY	181	ggacagggccctcgaagttgattggagttattaatatctactatgataatacaactaacac	240

Qy	Db	Query Match	Best Local Similarity	Matches	318: Conservative	78.5%: Pred.	0: Mismatches	87: Indels	0: Gaps
Qy	225	GCAAGAGCTCTAGAGTGGATTGGAATTATATAGTCTTACAAATGGTGAATACAGCTAAC	65.6%: Score 265.8; DB 1; Length 1767;						
Qy	241	cagaagtttaaggcgaagcccaacatgactgctgtatagaacagtcgacgacagcctatag							
Db	285	CCGAGGTTTAAGGGCAAGGCCACATGATCTGTATAGCAAAATCCCTCCACAGCCTATATG							
Qy	301	gaactagttctttgaagtcgaaatacggccgtttattactgttgaagaagcgccctg							
Db	345	GAACCTGCCAGATTGACATCTGAAAGATTCTCCATCTATTATCTGTGAAG--GGAGC							
Qy	361	tatatgactactggggtcgaagatgacccctgtccacgctctccca							
Db	402	AACCTTGACTACTGGGGCCAGGACGACACCTGTACAGTCTCTCA							
RESULT	4								
ID	V61363	V61363 standard; cDNA to mRNA; 1767 BP.							
AC	V61363:								
DC	18-JAN-1999	(first entry)							
DE	Anti-human Fas humanised antibody CH11 heavy chain HmuH cDNA.								
DE	Humanised antibody; Fas; CH11; monoclonal antibody; MA2; apoptosis;								
KW	autoimmune disease; rheumatoid arthritis; therapy; human;								
OS	antibody engineering; ds.								
KS	Homo sapiens.								
MS	Synthetic.								
FT	Key	Location/Qualifiers							
FT	slg_peptide	1..57							
FT	mat_peptide	/*tag= a							
FT		58..1764							
FT		/*tag= b							
PN	EP-866131-A2.								
PN	23-SEP-1998.								
PR	20-MAR-1998; 302113.								
PR	21-MAR-1997; JP-067938.								
PA	(SANY) SANKYO CO LTD								
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,								
PI	Yonehara S,								
DR	WPI: 98-482965/42.								
DR	P-PSDB; W11880.								
PT	Production of anti-Fas protein humanised antibodies - for use in								
PT	inducing apoptosis on Fas expressing cells in the treatment of								
PT	autoimmune diseases, especially rheumatoid arthritis								
PS	Example 3; Page 103-105; 187BP; English.								
CC	This cDNA sequence codes for a humanised anti-Fas antibody CH11								
CC	heavy chain (see W11880), designated HmuH. HmuH is based on the								
CC	light chain (see W11888) of murine anti-human Fas monoclonal								
CC	antibody CH11. The humanised sequence was designed following								
CC	selection of donor residues from CH11 to be grafted onto acceptor								
CC	molecule 21.28 CL. 2 Light chain sequences (see W11880-81) have								
CC	been designed, and each can be used in combination with any of 4								
CC	light chain sequences (see W11876-79) to provide novel, claimed								
CC	humanised CH11 IgM antibodies that lack a J chain. These humanised								
CC	anti-human Fas antibodies are capable of inducing apoptosis in cells								
CC	expressing Fas (e.g. synovialocytes) and are useful in the treatment								
CC	of autoimmune disease and chronic rheumatoid arthritis. DNA								
CC	sequences encoding the humanised antibodies are claimed, as are								
CC	vectors such as pRmuH5-1 including the HmuH nucleotide sequence,								
CC	and host cells such as Escherichia coli pRmuH5-1 (FERM BP-5865).								
SO	Sequence 1767 BP; 384 A; 368 C; 485 G; 350 T;								

Db	61	GTGAGCTTGTGACGCTGTGGGGCTGAGAGTGAAGAAAGCCGTGGGGCTCATGGAAGTTTCC	120
Qy	121	tgcgaagcttcggcctcacattactgatatgcatacagtggtgtgacaggtcct	180
Db	121		180
Qy	181	ggacaagccttcgtgatgtggtatataattactacatgataataaactaac	240
Db	181		240
Qy	241	cagaagtttaaggccaagggccacacatgactgtagacaagtcgaagcacagccatagt	300
Db	241		300
Qy	301	gaacttgattctttagagactgtagatacagggccggttattactgtgtcaagagcgccgtg	360
Db	301		360
Qy	361	tatttgactactgtgggtcaaggtacacctgtaccgcgtccctca	405
Db	361		405
RESULT	5		
V61364			
AC	V61364	standard; cDNA to mRNA; 1768 BP.	
DT	18-JAN-1999	(first entry)	
DE	Anti-human Fas humanised antibody CH11 heavy chain Hmum cDNA.		
KW	Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;		
KW	autoimmune disease; rheumatoid arthritis; therapy; human;		
OS	Homo sapiens.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1767	
FT		/*tag= a	
FT	sig_peptide	1..57	
FT		/*tag= b	
FT	mat_peptide	58..1764	
FT		/*tag= c	
PN	EP-866131-AZ.		
PD	23-SEP-1998.		
PR	20-MAR-1998; 3021113.		
PR	21-MAR-1997; JP-067938.		
PA	(SANY) SANKYO CO LTD.		
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,		
PI	Yonehara S;		
DR	WPI; 98-482965/42.		
PT	P-PSDB; W71881.		
PT	Production of anti-Fas protein humanised antibodies - for use in		
PT	inducing apoptosis on Fas expressing cells in the treatment of		
PT	autoimmune diseases, especially rheumatoid arthritis		
PS	Example 3; Page 108-110; 187pp; English.		
CC	This cDNA sequence codes for a humanised anti-Fas antibody CH11		
CC	heavy chain (see W71881), designated Hmum. Hmum is based on the		
CC	light chain (see W71888) of murine anti-human Fas monoclonal		
CC	antibody CH11. The humanised sequence was designed following		
CC	selection of donor residues from CH11 to be grafted onto acceptor		
CC	molecule 21.28 CL.		
CC	2 Light chain sequences (see W71880-81) have		
CC	been designed, and each can be used in combination with any of 4		
CC	light chain sequences (see W71876-79) to provide novel, claimed		
CC	humanised CH11 IgM antibodies that lack a J chain. These humanised		
CC	anti-human Fas antibodies are capable of inducing apoptosis in cells		
CC	expressing Fas (e.g. synovialocytes) and are useful in the treatment		
CC	of autoimmune disease and chronic Rheumatoid arthritis. DNA		
CC	sequences encoding the humanised antibodies are claimed, as are		
CC	vectors such as pMmu1-1 including the Hmum nucleotide sequence,		
CC	and host cells such as Escherichia coli pMmu1-1 (FERM BP-5864).		
SQ	Sequence	1768 BP; 387 A; 564 C; 485 G; 332 T;	

Query Match 65.6%; Score 265.8; DB 1; Length 1768;

Best Local Similarity 78.5%; Pred. No. 8.8e-68;
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

```

OY 1 atgggttggaactgtatatactctctcttctgtgtacacagcagctgagtgactccag 60
DB 1 ATGGGATGGAGTGGATCTTCTCTCTCCCTGTCAGAGTGCAGGCGCTCCACTCTGAG 60
OY 61 gccacgctgtcagctcgtggtcgtgagaaagcctgggagcctcagtgaggtc 120
DB 61 gccacgctgtcagctcgtggtcgtgagaaagcctgggagcctcagtgaggtc 120
OY 61 cttgcagcttctgcacgtctggcgctgagtgagaaagcctgggagcctcagtgaggtc 120
DB 61 cttgcagcttctgcacgtctggcgctgagtgagaaagcctgggagcctcagtgaggtc 120
OY 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
DB 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
OY 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
DB 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
OY 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
DB 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
OY 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
DB 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
OY 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
DB 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
OY 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
DB 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
OY 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
DB 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
OY 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
DB 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
OY 361 tatatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 405
DB 361 tatatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 405

```

RESULT 6

T42717

ID T42717 standard; DNA: 424 BP.

AC T42717.

DT 04-FEB-1997 (first entry)

DE Humc3 VH coding sequence.

KW Humc3 VH; BA6 antigen; human; milk fat globule; HMG; lactation;

KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;

KW breast membrane glycoprotein; therapy; immunotherapy; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT cds 11. 418

FT /*tag= a /product= Humc3 VH (BR-M version)

PD MO9608565-A2.

PD 21-MAR-1996.

PF 14-SEP-1995; U11683.

PF 16-SEP-1994; US-107868.

PR 07-JUN-1995; US-487598.

PA (CANCER) CANCER RES FUND CONTRA COSTA.

PI Certant R.T. Do Couto FUR, Peterson JA.

DR P-PSDB; W06442.

DR WPI; 96-17994/18.

PT Recombinant Mc3 antibody which binds BA6 antigen of HMG -

PT comprises a modified heavy or light chain variable region, useful in

PT the diagnosis and therapy of breast cancer

PS Claim 13; Fig 18; 91pp; English.

CC This sequence represents the coding sequence for the variable heavy (VH)

CC chain of the humanised murine antibody Humc3 VH. The Mc3 VH sequence was

CC humanised using the buried residue modification technique, where

CC important non-human framework residues are unaffected. The Mc3 antibody

CC binds to the BA6 antigen of the human milk fat globule (HMG). The milk

CC fat globule membrane is derived from the apical surface of the mammalian

CC epithelial cell during lactation, and therefore is a source for breast

CC membrane glycoproteins. The antibody can be used in an in vitro method

CC to detect a HMG antigen (or antigen fragment), and to diagnose the

CC presence of the antigen in a subject. The antibody can also be used to

CC deliver an agent to a target (within a subjects body), containing a HMG

CC antigen. The antibodies can also be used for diagnosis, prognosis, and

CC therapeutic applications of breast cancer. As the humanised antibodies

CC retain their high affinity binding to the antigen, they are useful for
CC immunodiagnostic and immunotherapeutic applications in humans.
SQ Sequence 424 BP; 106 A; 102 C; 112 G; 104 T;

Query Match 62.8%; Score 254.4; DB 1; Length 424;
Best Local Similarity 78.2%; Pred. No. 1.1e-64;
Matches 319; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

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OY 1 atgggttggaactgtatatactctctcttctgtgtacacagcagctgagtgactccag 60
DB 1 ATGGGATGGAGTGGATCTTCTCTCTCCCTGTCAGAGTGCAGGCGCTCCACTCTGAG 70
OY 61 gccacgctgtcagctcgtggtcgtgagaaagcctgggagcctcagtgaggtc 120
DB 61 gccacgctgtcagctcgtggtcgtgagaaagcctgggagcctcagtgaggtc 120
OY 61 cttgcagcttctgcacgtctggcgctgagtgagaaagcctgggagcctcagtgaggtc 130
DB 61 cttgcagcttctgcacgtctggcgctgagtgagaaagcctgggagcctcagtgaggtc 130
OY 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
DB 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
OY 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
DB 121 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 180
OY 131 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 190
DB 131 tgcagaagcttcggctacacattcattatgctatacagtggtgagagagctcct 190
OY 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
DB 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
OY 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 250
DB 181 ggcagggcctcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 250
OY 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
DB 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 300
OY 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 310
DB 241 cagaagtttaaggcagagccacaaatgactgagacaaagtcagagcagcctatag 310
OY 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
DB 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
OY 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
DB 301 gaactagttcttctgagatcgtgagagtaagcgcgtttattactgtgcaagagcgctcg 360
OY 361 ta---tatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgag 405
DB 361 ta---tatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgag 405
OY 371 tatatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 418
DB 371 tatatgagacttggtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 418

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RESULT 7

066702

ID 066702 standard; cDNA: 451 BP.

AC 066702.

DT 16-NOV-1994 (first entry)

DE DREG-200 Humanized antibody heavy chain variable region.

KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;

KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;

KW complementarily determining region; CDK; monoclonal antibody; Mab;

KW framework; light chain; heavy chain; variable domain;

KW monoclonal antibody; acceptor antibody Eu; transgenic animal; ss.

OS Mus sp.; Homo sapiens

FH Key Location/Qualifiers

FT cds 12. 434

FT /*tag= a

FT signal_peptide 12. 68

FT /*tag= b

FT mat_peptide 69. 431

FT /*tag= c

PD MO9412215-A.

PD 09-JUN-1994.

PF 30-NOV-1993; U11612.

PR 01-DEC-1992; US-983946.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Co MS;

DR WPI; 94-199974/24.

DR P-PSDB; R55556.

PT New humanised antibody specific for L-selectin - with murine CDR

PT and human framework regions, inhibits binding of neutrophils to

PT endothelial cells and useful for treating or preventing

PT inflammation

PS Disclosure; Fig. 3B; 60pp; English.

CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs

CC corresponding to those of mouse Mab DREG-200 and heavy and light

CC chain variable region frameworks of the human acceptor antibody Eu.

Db 141 TGCAGAGCTTGTGCTACACCTTCCACGACTGTGATGCGTGGTAAACAGGCCCT 200
 Qy 181 ggaacaggccctcgagtgatgagtgatattactatgataatacaactaac 240
 Db 201 GGACAGGCGCTTGAGTGGATGGAGATTGATCTTCTGTACTACTATTAACCTAACAT 260
 Qy 241 cagaagtttaaggccaagcaatgactgtagacaagtgaagcagacagcctatg 300
 Db 261 CAAAGATTCAAGGCCAAGGCCACATGTACTATAGACATCAATCATTAGCACGCTACATG 320
 Qy 301 gaactagttcttgagatctgagatacggcgcttattactgtagaaga----- 351
 Db 321 GAGCTCAGACGCTGAGATCTGAGGACACGCGGCTATTACTGTGCAAGAAATAGGAGAC 380
 Qy 352 -----gcggcctggtatattgactactgagtgagtgacccctgtccacgcttctca 405
 Db 381 TATAGTAACAACCTGTAAGTGTCTGGGCGGAGAGGAGACCCTGTCACCGTCTCTCA 440
 RESULT 9
 ID V70104 standard: cDNA to mRNA: 457 BP.
 AC V70104;
 DE 15-MAR-1999 (first entry)
 KW Anti-Fas humanised antibody HFE7A heavy chain variable region cDNA.
 KW HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A: autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 21..458
 FT FT /*tag- a
 FT 21..77
 FT sig_peptide /*tag- b
 FT 78..455
 FT mat_peptide /*tag- c
 PN A09859701-A.
 PD 08-OCT-1998.
 PE 30-MAR-1998: 059701.
 PR 08-OCT-1997: JP-276064.
 PR 01-APR-1997: JP-082953.
 PR 25-JUN-1997: JP-169088.
 PA (SANY) SANKYO CO LTD.
 PI Akiro S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobuhisa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR P-PSDB: W83038.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Example 3; Page 206-207; 292pp; English.
 CC This nucleotide sequence codes for the VD type humanised heavy
 CC chain variable region (see W83038) of murine anti-human Fas
 CC monoclonal antibody HFE7A. It was utilised in the construction
 CC of a claimed humanised HFE7A heavy chain (see V70079). The
 CC invention provides methods for producing humanised antibodies by
 CC culturing host cells. Humanised versions of HFE7A (see W83031-37)
 CC are capable of inducing apoptosis in abnormal cells expressing Fas,
 CC and of inhibiting Fas-induced apoptosis in normal cells. Humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,

CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 457 BP; 113 A; 117 C; 126 G; 101 T;
 Query Match 61.4%; Score 248.8; DB 1; Length 457;
 Best Local Similarity 76.9%; Pred. No. 4.7e-63;
 Matches 323; Conservative 0; Mismatches 82; Indels 15; Gaps 1;
 Qy 1 atggtgtgaactgtatcatcttcttgcgttaccacagcagtgatccacag 60
 Db 21 ATGGAGTGGAGCTGTGATCAATCCCTTCTTGAGCAACAGCTACAGTCTCCAG 80
 Qy 61 gtccagctggtgagctctgggtgagtgaaagcctgggagctcagtgaaagtgtcc 120
 Db 81 GTCCAACTGTGCTGAGTGTGGGCTGAGTCAAGACCTGGGCTTCACTGAAGTGTCC 140
 Qy 121 tgcgaagcttcggctcacacatctacgtattatgtatatacagtgagagctcct 180
 Db 141 TGCAGAGCTTGTGCTACACCTTCCACGACTGTGATGCGGTTAAACAGGCCCT 200
 Qy 181 ggaacaggccctcgagtgatgagtgatattactatgataatacaactaac 240
 Db 201 GGACAGGCGCTTGAGTGGATGGAGATTGATCTTCTGTACTACTATTAACCTAACAT 260
 Qy 241 cagaagtttaaggccaagccacaatgactgtagacaagtgaagcagacagcctatg 300
 Db 261 CAAAGATTCAAGGCCAAGGCCACATGTACTATAGACATCAATCATTAGCACGCTACATG 320
 Qy 301 gaactagttcttgagatctgagatacggcgcttattactgtagaaga----- 351
 Db 321 GAGCTCAGACGCTGAGATCTGAGGACACGCGGCTATTACTGTGCAAGAAATAGGAGAC 380
 Qy 352 -----gcggcctggtatattgactactgagtgagtgacccctgtccacgcttctca 405
 Db 381 TATAGTAACAACCTGTAAGTGTCTGGGCGGAGAGGAGACCCTGTCACCGTCTCTCA 440
 RESULT 10
 ID V70079 standard: DNA; 2077 BP.
 AC V70079;
 DE 15-MAR-1999 (first entry)
 KW Anti-Fas humanised antibody HFE7A heavy chain DNA.
 KW HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A: autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; ds.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 27..2042
 FT FT /*tag- a
 FT 28..83
 FT sig_peptide /*tag- b
 FT 1..741
 FT FT /*tag- c
 FT 742..1132
 FT intron

QY 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 DB 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 QY 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 DB 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 QY 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240
 DB 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240
 QY 241 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 300
 DB 241 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 300
 QY 301 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 360
 DB 301 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 360
 QY 361 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 405
 DB 361 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 405

RESULT 12

V37264 standard; cDNA: 405 BP.

AC V37264:
 DT 10-SEP-1998 (first entry)
 DE cDNA encoding a variable region of an anti-Fas antibody heavy chain.
 KW Variable region; heavy chain; anti-Fas antibody; human; mouse;
 KM immunoglobulin G; IgG; light chain; treatment; diagnosis;
 KN autoimmune disease; ss.
 OS Mus sp.
 PN J10165178-A.
 PD 23-JUN-1998.
 PF 01-JUL-1997: 191769.
 PR 09-OCT-1996: JP-268737.
 PR 02-JUL-1996: JP-172228.
 PA (IGAK-) IGAKU SEIBUTSUGAKU KENRYUSHO KK.
 DR WPI: 98-406105/35.
 PT DNA encoding, e.g., variable region of anti-Fas antibody - useful
 PT for, e.g., diagnosis and treatment of auto-immune diseases
 PS Claim 2; Page 12; 16pp; Japanese.
 CC The present sequence encodes a variable region of the heavy chain of an
 CC anti-Fas antibody. The constant region of the heavy chain is derived
 CC from human immunoglobulin G (IgG). The anti-Fas antibody can be used
 CC for the treatment and diagnosis of autoimmune diseases.
 SQ Sequence 405 BP: 103 A; 102 C; 102 G; 98 T;

Query Match

60.1%; Score 243.4; DB 1; Length 405;

Best Local Similarity 75.1%; Pred. No. 1.7e-61;

Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttcgtgtacacagctcaggtgtgactccag 60
 DB 1 atgggttggaactgtatcatctcttcgtgtacacagctcaggtgtgactccag 60
 QY 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 DB 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 QY 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 DB 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 QY 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240
 DB 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240

QY 241 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 300
 DB 241 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 300
 QY 301 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 360
 DB 301 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 360
 QY 361 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 405
 DB 361 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 405

RESULT 13

T88869 standard; DNA: 1773 BP.

AC T88869:
 DT 15-APR-1998 (first entry)
 DE H chain subunit of Fas specific antibody coding sequence.
 KW Fas; antibody; human; immunoglobulin; variable region; rheumatism;
 KM autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain;
 KN complementarily determining region; ss.
 OS Mus musculus.
 PN EP-79891-A1.
 PD 08-OCT-1997.
 PF 27-MAR-1997: 302415.
 PR 01-APR-1996: JP-078570.
 PA (SANY) SANKYO CO LTD.
 PI Ichikawa K, Nakahara K, Serizawa N, Yonehara S;
 DR WPI: 97-482673/45.
 DR P-PSDB: W31751.
 PT Anti-Fas recombinant antibodies - useful for treating auto-immune
 PT diseases, especially rheumatoid arthritis
 PS Claim 18; Page 29-31; 72pp; English.
 CC This sequence represents the coding sequence for the heavy chain of the
 CC protein of the invention. The protein of the invention is a recombinant
 CC protein (A), that comprises at least one region corresponding to an
 CC immunoglobulin (Ig) variable region which enables the protein to
 CC recognize and specifically bind to an antigen, preferably human Fas, and
 CC has substantially no more immunogenicity in a human patient than a human
 CC antibody. The proteins are useful for treating autoimmune diseases,
 CC especially rheumatism (rheumatoid arthritis). (A) is based on a murine
 CC monoclonal antibody. As the protein lacks the constant region, it has
 CC substantially no more immunogenicity in the human patient than a human
 CC antibody.
 SQ Sequence 1773 BP: 455 A; 512 C; 416 G; 390 T;

Query Match

60.1%; Score 243.4; DB 1; Length 1773;

Best Local Similarity 75.1%; Pred. No. 2.6e-61;

Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttcgtgtacacagctcaggtgtgactccag 60
 DB 1 atgggttggaactgtatcatctcttcgtgtacacagctcaggtgtgactccag 60
 QY 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 DB 61 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 120
 QY 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 DB 121 tgcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 180
 QY 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240
 DB 181 gtcacagctgctgacatctgggctgagtgaaagacgctggagacgtcaagtgtctc 240

Db 181 GGAAGAGCCCTGAGTGGATTGGATATATTATTCCTTACATGGTGGTACTGGCTACAC 240
 QY 241 caaagaatttaaggcaagggcacaatgactgtagaagaagcagagcagcctatacg 300
 Db 241 CAGAAGTTCAGAGCAAGGACACATTGACTGTGACAAATTCCTCCACACAGCCTACATG 300
 QY 301 gaactatgtctcttgaatctgagataggaagcagcgtttattactgtgaagagcgccctg 360
 Db 301 GACTCCGCGAGCCTGACATGTGAGGACTGTGAGACTGTATTAATCTGCAAGAGATTACTAT 360
 QY 361 tataatgactactggtgggtcaaggtacccctgtcaacgcgtccctca 405
 Db 361 GCTATGAGACTACTGGGGTCAAGGAACCTCAGTACCGCTCTCTCA 405

RESULT 14

V66735 ID V66735 standard; cDNA to mRNA; 1773 BP.

AC V66735;
 DT 18-JAN-1999 (first entry)
 DE Anti-human Fas monoclonal antibody CH11 heavy chain cDNA.
 KW Humanised antibody; Fas; CH11; monoclonal antibody; MAD; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
 KW antibody engineering; ds.
 OS Synthetic.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT sig_peptide 1..57
 FT /*tag- a
 FT mat_peptide 58..1770
 FT /*tag- b
 PN EP-866131-A2.
 PD 23-SEP-1998.
 PE 20-MAR-1998; 302113.
 PR 21-MAR-1997; JP-067938.
 PA (SANY) SANKYO CO LTD.
 PI Haruyama H, Nakahara K, Serizawa N, Takahashi T,
 PI Konehara S;
 PI MPI: 98-482965/42.
 DR P-P5DB; W71888.
 PT Production of anti-Fas protein humanised antibodies - for use in
 PT inducing apoptosis on Fas expressing cells in the treatment of
 PT autoimmune diseases, especially rheumatoid arthritis
 PS Reference Example 4; Page 55-58; 187pp; English.
 CC This cDNA sequence codes for the heavy chain (see W71888) of
 CC mouse anti-human Fas monoclonal antibody CH11. It was obtained
 CC from CH11 hybridoma cDNA by PCR amplification (see V66675-76).
 CC The heavy chain cDNA in pCR3-H123 is deposited as FERM BP-5427.
 CC The invention relates to novel humanised antibodies comprising
 CC humanised light and heavy chains (see W71876-81) of CH11. These
 CC humanised anti-human Fas antibodies are capable of inducing
 CC apoptosis in cells expressing Fas (e.g. synovialocytes) and are
 CC useful in the treatment of autoimmune disease and chronic
 CC rheumatoid arthritis.
 SQ Sequence 1773 BP; 455 A; 512 C; 416 G; 390 T;

Query Match 60.1%; Score 243.4; DB 1; Length 1773;
 Best Local Similarity 75.1%; Pred. No. 2.6e-61;
 Matches 304; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagttacaggtgtcactccag 60
 Db 1 ATGGGATGGAGCTGGATCTTCTCTCTCTCTCTGTCAGCAACTGCAAGGCTCCCTGAG 60
 QY 61 gtccagctgtgtcagctgtcgtgagtggaagcctgtggagctcagtaaggtgtcc 120
 Db 61 GTCCAGCTTTCAGAGCTGACGACCTGAGCTGTGTAACCTGGGGCTCTCAGTAAGTATCC 120
 QY 121 tgcgaagcttcgcgtacacattcatgattatgctatcacagtggtgtgagacagctct 180
 Db 121 TGCGAAGCTTCTGCTGATACACATTCACATGACATGACATGAGTGGTGAACGAGGCAT 180

QY 181 ggaagggctcgcagtgagtgagtgagttatataattactactatgataataacac 240
 Db 181 GGAAGAGCCTTAGCTGATGGATTGGATATATTATTCCTTACATAGTGGTACTGGCTACAC 240
 QY 241 caaagaatttaaggcaagggcacaatgactgtagaagaagcagagcagcctatacg 300
 Db 241 CAGAAGTTCAGAGCAAGGACACATTGACTGTGACAAATTCCTCCACACAGCCTACATG 300
 QY 301 gaactatgtctcttgaatctgagataggaagcagcgtttattactgtgaagagcgccctg 360
 Db 301 GACTCCGCGAGCCTGACATGTGAGGACTGTGAGACTGTATTAATCTGCAAGAGATTACTAT 360
 QY 361 tataatgactactggtgggtcaaggtacccctgtcaacgcgtccctca 405
 Db 361 GCTATGAGACTACTGGGGTCAAGGAACCTCAGTACCGCTCTCTCA 405

RESULT 15

V88433 ID V88433 standard; cDNA; 478 BP.

AC V88433;
 DT 12-FEB-1999 (first entry)
 DE EST clone GF196.
 KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
 KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
 KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
 KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 OS Homo sapiens.
 PN WO9845437-A2.
 PD 15-OCT-1998.
 PE 10-APR-1998; U06956.
 PR 10-APR-1997; US-837312.
 PA (GBMR) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie LA, Spaulding V, Treacy M;
 DR MPI: 99-070078/06.
 PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries
 PS Claim 1; Page 395; 641pp; English.
 CC The present sequence represents an expressed sequence tag (EST), and is
 CC a polynucleotide of the invention. The polynucleotides of the invention
 CC are all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene
 CC therapy.
 SQ Sequence 478 BP; 123 A; 126 C; 125 G; 104 T;

Query Match 59.8%; Score 242.2; DB 1; Length 478;
 Best Local Similarity 76.0%; Pred. No. 3.9e-61;
 Matches 317; Conservative 0; Mismatches 88; Indels 12; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagttacaggtgtcactccag 60
 Db 47 ATGGGATGGAGCTGATATCATCTCTTTTGGTACCAACGCTAACAGGTCCACTCCAG 106
 QY 61 gtccagctgtgtcagctgtcgtgagtggaagcctgtggagctcagtaaggtgtcc 120
 Db 107 GTCCAGCTTTCAGAGCCTCGGGGCTGAGCTGTGTAACCTGGGGCTCTCAGTAAGTGTCC 166
 QY 121 tgcgaagcttcgcgtacacattcatgattatgctatcacagtggtgtgagacagctct 180
 Db 167 TGCGAAGCTTCTGCTGATACACATTCACACGATGAGATGACACTGGTGAACGAGGCCT 226

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OY 181 egacagggccctcgagtgatggagttatlaataattactatgataatacaactacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 227 GGACAAGGCGCTTGAGTGGATGGATGATTCCTAATAGTGTAGTACTAATACAAT 286
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 cagaagtttaaggcgaagcccaatgaacttagacaagtcgacgagcagcctatatg 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 287 GAGAAGTTCMAAGACAGGCGCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 gaacttaagttcttagagatcgaagataagcgcttattactgtgcaagag----- 352
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 347 CAACTCAGCAGCCTGACATCTGAGGACTCTGCGTCTTATTACTGTGCAAGGACAGCTCA 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 353 ----cgacctggtatatactgactactcgggtcaaggtacccctgtcaccgtctcctca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 407 GGCTACGACTATGCTATGAGTACTGCGGTCAAGGAACCTCAGTCACCGTCTCTCA 463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: August 27, 2000, 06:25:32
Job time: 1929 sec

 W O R L D
 (TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 7 18:59:31 2000; Maspar time 12.47 Seconds
 510.767 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-249-011-6
 Description: (1-135) from US09249011.pep
 Perfect Score: 999
 Sequence: 1 MGNMCIFFLVTTATGVHSQ.....ARAAWMDYMGQGTTLTVSS 135

Scoring table:
 PAM 150
 Gap 11
 Searched: 142080 seqs, 47172406 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r64
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.058; Variance 92.001; scale 0.457

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	733	73.4	136	1	HVMSB1	1g heavy chain precu
2	717	71.8	135	2	S49530	anti-Sm antibody VH c
3	708	70.9	138	2	E32513	1g heavy chain precu
4	705	70.6	135	2	A30577	1g heavy chain precu
5	694	69.5	141	2	JL0076	1g heavy chain precu
6	685	68.6	137	2	H32513	1g heavy chain precu
7	683	68.4	131	2	A27472	1g heavy chain precu
8	683	68.4	137	1	G2M543	1g heavy chain precu
9	683	68.4	139	2	A27609	1g heavy chain precu
10	680	68.1	150	2	PN0444	1g heavy chain V regi
11	679	68.0	139	2	HMS18	1g heavy chain V regi
12	678	67.9	136	2	PL0208	1g heavy chain precu
13	676	67.7	136	2	S31600	1g heavy chain precu
14	674	67.5	137	2	F29380	1g heavy chain precu
15	670	67.1	140	2	T01407	1g heavy chain precu
16	667	66.8	137	2	E29380	1g heavy chain (myelo
17	666	66.7	138	1	HVMS7	1g heavy chain precu
18	665	66.6	136	2	B47159	1g heavy chain V regi
19	665	66.6	138	2	S21810	1g heavy chain V regi
20	661	66.2	135	2	FS0057	1g heavy chain precu
21	660	66.1	151	2	PL0011	1g heavy chain precu
22	659	66.0	117	1	HVMS02	1g heavy chain precu
23	658	65.9	474	2	S25057	1g gamma-2b chain - m

24	657	65.8	134	2	S21916	1g heavy chain V regi
25	656	65.7	160	2	PL0105	anti-PR2 erythrocyte
26	655	65.6	140	2	S04575	1g heavy chain precu
27	654	65.5	131	2	S21824	1g heavy chain precu
28	646	64.7	117	1	HVMS3	1g heavy chain precu
29	643	64.4	110	2	PH1482	1g heavy chain V regi
30	641	64.2	117	2	S18553	1g heavy chain V regi
31	639	64.0	166	2	PL0012	1g heavy chain precu
32	638	63.9	118	2	S36265	1g heavy chain V regi
33	637	63.8	117	2	S18551	1g heavy chain V regi
34	637	63.8	140	1	HVMS67	1g heavy chain precu
35	635	63.6	116	2	PH0959	1g heavy chain V regi
36	635	63.6	132	2	S31596	1g heavy chain V regi
37	634	63.5	139	2	PS0042	1g heavy chain precu
38	634	63.5	140	2	PH1484	1g heavy chain precu
39	633	63.4	136	2	JL0077	1g heavy chain V regi
40	630	63.1	117	1	HVMS23	1g heavy chain precu
41	628	62.9	138	2	PH0105	anti-digoxin transfec
42	628	62.7	117	2	S31680	1g heavy chain V regi
43	626	62.7	117	1	HVH035	1g heavy chain precu
44	626	62.7	133	2	PC1155	1g heavy chain precu
45	625	62.6	469	2	S37483	1g gamma-2a chain - m

ALIGNMENTS

RESULT 1
 ENTRY HVMSB1 #type complete
 TITLE 1g heavy chain precursor V region (BCL1) - mouse
 ORGANISM Mus musculus #common_name house mouse
 DATE 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 22-Jun-1999

ACCESSION A02042
 REFERENCE A02042
 #authors Knapp, M.R.; Liu, C.P.; Newell, N.; Ward, R.B.; Tucker, P.W.; Strober, S.; Blattner, F.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1982) 79:2996-3000
 #title Simultaneous expression of immunoglobulin mu and delta heavy chains by a clone B-cell lymphoma: a single copy of the V-H gene is shared by two adjacent C-H genes.

#cross-references M01D:8222262
 #accession A02042
 ##molecule_type mRNA
 ##residues 1-136 #label KNA
 ##cross-references GB:J00494; NID:q195010; PID:AAA38130.1; PID:q195011
 ##note the sequence was determined from the differentiated gene

GENETICS
 #introns 16/1
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE
 1-19
 20-136

SUMMARY
 #length 136 #molecular-weight 15078 #checksum 7917

Query Match 73.4%; Score 733; DB 1; Length 136;
 Best Local Similarity 72.1%; Pred. No. 3.81e-111;
 Matches 98; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Db	1	MGNMCIFFLVTTATGVHSQVLOVQSGEYVVRGVYSKCSKSGTFTDYAHMWKQSH	60
QY	1	MGNMCIFFLVTTATGVHSQVLOVQSGEYVVRGVYSKCSKSGTFTDYAHMWKQSH	60
Db	61	AKSLEWIGVISTYNGNTSYNOKFKGKATMTVDSSSTVHMLRLTSEDSANLYCARYG	120
QY	61	GQGLEWIGVINITYNDNTNNQKFKATMTVDKSTRAVHMLSLSEDTAVYYCARA-A	119
Db	121	NYFDYMGQGTTLTVSS	136
QY	120	WYMDYMGQGTTLTVSS	135

Db	QY	Db	QY	RESULT	ENTRY	TITLE	ORGANISM	DATE	ACCESSIONS	REFERENCE	#authors	#journal	#title	#cross-references	#accession	#status	#molecule-type	#residues	#cross-references	KEYWORDS	FEATURE	SUMMARY	Query Match	Best Local Match	Matches
61	GOGLEWIGTGNITVSSSTNNNEKFKATITVDTSSSTAYMOLSLTSDSAVYYCARL	120	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	70.6%	Score 705; DB 2; Length 135;	71.98%;
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																	71.98%;	Pred. No. 6,80e-106;	
61	GOGLEWIGVINIYDNTNNOKFKGKATMTVDKSTAYMELSLRSDAYVYCARAA	119	120	4	A30577	Ig heavy chain precursor V region (MR10) - mouse (fragment)																			

KEYWORDS		heterotetramer; immunoglobulin
FEATURE		
1-19		#domain signal sequence #status predicted #label SIC\
20-141		#product Ig heavy chain #status predicted #label MARY
34-117		#domain immunoglobulin homology #label IMV\
50-54		#region complementarity-determining 1\
69-85		#region complementarity-determining 2\
123-135		#region J2 segment\
136-141		#region C
SUMMARY	#length 141	#checksum 8784
Query Match	69.5%;	Score 694; DB 2; Length 141;
Best Local Similarity	69.6%;	Pred. No. 7, 81e-104;
Matches	91; Conservative	23; Mismatches 18; Indels 0; Gaps 0;
Db	1 MGMSWIFLEATATGVSQVOYLQDPGAELVYKSGAKSLCKASGYFTSYMMHWKQP	60
Oy	1 MGMNCIIEFLVTATGVSHQVOLVGSAEVRKKRGSSVKVCSKASGYFTDPAIQWRQAP	60
Db	61 GGGLGWIGIDRNSGGTKRKNEKSKATITLVKPPSSATVAWQLSLSFSDSAVYYCAREGP	120
Oy	61 GGGLGWIGINITYDNTNNOKEKGRATMTVDKSTPAYMELSSLREDDTAIVYYCARAAW	120
Db	121 AGDYWGOGTTLTVSS	135
Oy	121 YMDYWGOGTTLTVSS	135
RESULT	6	
ENTRY	H32513	#type complete
TITLE	Ig heavy chain precursor V region (BXW16) - mouse	
ORGANISM	f[ormal_name Mus musculus v[common_name house mouse	
DATE	21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999	
ACCESSIONS	H32513	
REFERENCE	A94689	
Authors	Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.	
#journal	J. Clin. Invest. (1988) 82:852-860	
#title	Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.	
#cross-references	MUID:88331394	
#accession	H32513	
#molecule_type	DNA	
#residues	1-137 #label KOF	
#cross-references	GB:M20831; NID:g196949; PIDN:AAA38848.1; PTD:g196950	
CLASSIFICATION	#superfamily Immunoglobulin V region; Immunoglobulin heterotetramer; immunoglobulin	
KEYWORDS	#length 137 #molecular-weight 15108 #checks 816	
SUMMARY		
Query Match	68.6%;	Score 685; DB 2; Length 137;
Best Local Similarity	66.4%;	Pred. No. 3, 77e-102;
Matches	91; Conservative	26; Mismatches 18; Indels 2; Gaps 2;
Db	1 MGMSWIFLELAVTGAGVSEHIOLOQSGAEELVYKSGAKSLCKASGYFTGYNNMWKQSH	60
Oy	1 MGMNCIIEFLVTATGVSHQVOLVGSAEVRKKRGSSVKVCSKASGYFTDPAIQWRQAP	60
Db	61 GKSLDWIGNINDPYGSTYNOKFKGKATITLVKSSSTAYWQLNSLTSEDASVYYCARKNY	120
Oy	61 GGGLGWIGINITYDNTNNOKEKGRATMTVDKSTPAYMELSSLREDDTAIVYYCAR-A-	118
Db	121 GSPFDYWOGTTLTVSS	137
Oy	119 AMYMDYWGOGTTLTVSS	135
RESULT	7	
ENTRY	A27472	#type fragment
TITLE	Ig heavy chain precursor V region (1B9) - mouse (fragment)	
ORGANISM	f[ormal_name Mus musculus v[common_name house mouse	

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DATE          16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
              18-Oct-1996
ACCESSIONS    A27472
REFERENCE      Lih, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
#authors      Gene (1987) 54:33-40
#journal       Expression of mouse: human immunoglobulin heavy-chain cDNA in
#title         lymphoid cells.
               lymphotoid cells.
#cross-references M0ID:8277450
#accession     A27472
CLASSIFICATION ##molecule_type mRNA
                #residues 1-131 ##label Liu
KEYWORDS        #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE         heterotetramer; immunoglobulin
1-19            #domain signal sequence #status predicted #label SIG\
5-54            #region complementarity-determining 1\
20-131         #product Ig heavy chain V region IEG #status predicted
                #label MAR\
34-117         #domain immunoglobulin homology #label IMM\
69-85          #region complementarity-determining 2\
118-125        #region complementarity-determining 3
SUMMARY         #length 131 #checksum 1501

Query Match    68.4%; Score 683; DB 2; Length 131;
Best Local Similarity 70.5%; Pred. No. 8,92e+102;
Matches 93; Conservative 18; Mismatches 18; Indels 3; Gaps 3;

Db 1 MGMSYILFLVATATDVHSGVOLQPGALFLVRGASVKRLSCASGYFTSYWMHWKORP 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 1 MGNWCIIFLVLTAITGVHSOYLQGLAAYKKFGSSVAVKSCASSYTITTDIAIQWRAP 60
   |MGNWCIIFLVLTAITGVHSOYLQGLAAYKKFGSSVAVKSCASSYTITTDIAIQWRAP 60

Db 61 GGQIDWIGELINSGRNTNNEKRKNATLLTVDKSSSTAYMOLSLTSBDSAVYCCASYD 120
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 61 GQGLEMIVGINITYDDWTNNQKKRKATMTVDKSTAYMELSLRSBDTAVYYCAR-A- 118
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 121 DMF-AIYWGGDTL 131
   |:|||||:
Qy 119 AWYMDYWGOGTL 130

RESULT 8
ENTRY   GZMS43           #type complete
TITLE   Ig heavy chain precursor V region (S43) - mouse
ORGANISM Mus musculus #common_name house mouse
DATE    02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
        22-Jun-1999
ACCESSIONS A02038
REFERENCE   A02038
#authors    Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.;
             Rajewsky, K.; Baltimore, D.
#journal     Cell (1981) 24:625-637
#title       Heavy chain variable region contribution to the NP(b) family
             of antibodies: somatic mutation evident in a gamma2a
             variable region.
#cross-references M0ID:81234548
#accession   A02038
                ##molecule_type mRNA
                ##residues 1-137 ##label BOT
#cross-references GB:J00539; NID:g195118; PIDN:AAA8172.1; PID:g195119
                the gamma-2a chain mRNA was cloned from a hybridoma
                making antibodies to the hapten
                (4-hydroxy-3-nitrophenyl)acetyl (NPb antibodies)
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE         heterotetramer; immunoglobulin
1-19            #domain signal sequence #status predicted #label SIG\
20-137         #product Ig heavy chain V region (S43) #status predicted
                #label MAR\
34-117         #domain immunoglobulin homology #label IMM\
118-122        #region D segment\
123-137        #region J segment (JH2)
SUMMARY         #length 137 #molecular-weight 15200 #checksum 474

```

Query Match 68.4%; Score 683; DB 1; Length 137;
 Best Local Similarity 67.2%; Pred. No. 8.92e-102;
 Matches 92; Conservative 23; Mismatches 20; Indels 2; Gaps 1;

Db 1 MGNCMIFLFLATATGVSQVLOQPGAEVYKPCASVYKSLCKASGYFTDTAIDMWRQAP 60
 1 MGNCMIFLFLATATGVSQVLOQPGAEVYKPCASVYKSLCKASGYFTDTAIDMWRQAP 60
 1 MGNCMIFLFLATATGVSQVLOQPGAEVYKPCASVYKSLCKASGYFTDTAIDMWRQAP 60

QY 61 GQGLEWIGVINYIDNNTNFKGKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118
 61 GQGLEWIGVINYIDNNTNFKGKATMTVDKSTAYMELSLRSDTAIVYCAR--A 118

Db 121 GRXPDMGCGTTLTVSS 137
 121 GRXPDMGCGTTLTVSS 137
 119 AWMDYWGCGTLTVSS 135

RESULT 9
 ENTRY A27609 #type complete
 TITLE Ig heavy chain precursor V region (129) - mouse
 ORGANISM Mus musculus #common_name house mouse
 DATE 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999

ACCESSIONS A27609
 REFERENCE A27609 Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
 #authors J. Immunol. (1988) 140:1676-1684
 #journal I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch.
 #title alter H chain switch.
 #cross-references M01D:88154467
 #accession A27609
 #molecule_type DNA
 #residues 1-139 #label KLE
 #cross-references EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g533992

GENETICS 16/1
 #introns
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 1-19
 20-139 #domain signal sequence #status predicted #label SIG
 #product Ig heavy chain V region 129 #status predicted
 #label VAR
 #domain immunoglobulin homology #label IMM
 SUMMARY 34-117
 #length 139 #molecular_weight 15643 #checksum 5928

Query Match 68.4%; Score 683; DB 2; Length 139;
 Best Local Similarity 68.3%; Pred. No. 8.92e-102;
 Matches 95; Conservative 25; Mismatches 15; Indels 4; Gaps 3;

Db 1 MGNCMIFLFLSTAGVLSQVLOQSGPELVKPGASVYKSCASGYFTDVVMHVRQSN 60
 1 MGNCMIFLFLSTAGVLSQVLOQSGPELVKPGASVYKSCASGYFTDVVMHVRQSN 60
 1 MGNCMIFLFLSTAGVLSQVLOQSGPELVKPGASVYKSCASGYFTDVVMHVRQSN 60

QY 61 GKSLEWIGVINYIDNNTNFKGKATLTVDKSSSTAYMOLNLTSDSAVYVCARTSY 120
 61 GQGLEWIGVINYIDNNTNFKGKATMTVDKSTAYMELSLRSDTAIVYCAR-A- 118

Db 121 YSTYAMDYWGCGTSVTVSS 139
 121 YSTYAMDYWGCGTSVTVSS 139
 119 -AWY-MDYWGCGTLTVSS 135

RESULT 10
 ENTRY PN0444 #type fragment
 TITLE Ig heavy chain V region precursor - human (fragment)
 ORGANISM Homo sapiens #common_name man
 DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

ACCESSIONS PN0444
 REFERENCE PN0444 Kaluza, B.; Betzl, G.; Shao, H.; Diamantsehn, T.; Weidle, Kaluza, B.; Betzl, G.; Shao, H.; Diamantsehn, T.; Weidle,

U.H.
 Gene (1992) 122:321-328
 A general method for chimerization of monoclonal antibodies
 by inverse polymerase chain reaction which conserves
 authentic N-terminal sequences.

#journal 122:321-328
 #title A general method for chimerization of monoclonal antibodies
 by inverse polymerase chain reaction which conserves
 authentic N-terminal sequences.
 #cross-references M01D:93138402
 #accession PN0444
 #molecule_type mRNA
 #residues 1-150 #label KAL
 #cross-references GB:102346

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS heterotetramer; immunoglobulin
 FEATURE 1-19
 20-150 #domain signal sequence #status predicted #label SIG
 #product Ig heavy chain V region #status predicted
 #label VAR
 #domain variable region #label VRG
 SUMMARY 20-117
 #length 150 #checksum 9720

Query Match 68.1%; Score 680; DB 2; Length 150;
 Best Local Similarity 66.4%; Pred. No. 3.25e-101;
 Matches 91; Conservative 26; Mismatches 18; Indels 2; Gaps 2;

Db 1 MEMSWIFLFLISGTAGVLSQVLOQSGAEVYKPCGTYSKICKASGYFTDYNMDWKQSH 60
 1 MEMSWIFLFLISGTAGVLSQVLOQSGAEVYKPCGTYSKICKASGYFTDYNMDWKQSH 60
 1 MGNCMIFLFLATATGVSQVLOQSGAEVYKPCGSVYKSCASGYFTDTAIDMWRQAP 60

QY 61 GKSLEWIGVINYIDNNTNFKGKATMTVDKSSSTAYMELSLRSDTAIVYCAR--A 120
 61 GQGLEWIGVINYIDNNTNFKGKATMTVDKSTAYMELSLRSDTAIVYCARAAW 120

Db 121 PYGMDYWGCGTSVTVSS 137
 121 PYGMDYWGCGTSVTVSS 137
 121 -Y-MDYWGCGTLTVSS 135

RESULT 11
 ENTRY MHMS18 #type complete
 TITLE Ig heavy chain precursor V region (B1-8) - mouse
 ORGANISM Mus musculus #common_name house mouse
 DATE 02-Apr-1992 #sequence_revision 02-Apr-1992 #text_change 22-Jun-1999

ACCESSIONS A90809; A22769; A02034; A02036
 REFERENCE A90809 Bothwell, A.L.M.; Pasikind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
 #authors Bothwell, A.L.M.; Pasikind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
 #journal Cell (1981) 24:625-637
 #title Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.
 #cross-references M01D:81234548
 #accession A90809
 #molecule_type DNA
 #residues 1-139 #label B18
 #cross-references GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
 #accession B90809
 #molecule_type DNA
 #residues 1-117 #label 1862
 #note the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl (NPb antibodies) the 186-2 germline gene was cloned from a library of C57BL/6 DNA

REFERENCE A90971
 #authors Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
 #journal EMBO J. (1982) 1:635-640
 #title Immunoglobulin V region variants in hybridoma cells. II. Recombination between V genes.
 #cross-references M01D:84236026
 #accession A22769
 #molecule_type protein

##residues 20-139 ##label DIL
##note the V region of the B1-8 delta chain, derived as a spontaneous class switch variant from the IGM-producing B1-8 hybridoma, was partially sequenced; the sequence is identical with the V region of the mu chain

GENETICS
#introns 16/1
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin

FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
20-139 #product Ig kappa chain V region (B1-8) #status experimental #label MAT\
34-117 #domain immunoglobulin homology #label IMM\
118-124 #region D segment\
125-139 #region J segment (JH2)
#length 139 #molecular-weight 15419 #checksum 5229

SUMMARY

Query Match
Best Local Similarity 68.3%; Pred. No. 4.99e-101;
Matches 95; Conservative 24; Mismatches 16; Indels 4; Gaps 1;

Db
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Qy
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Db
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Qy
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Db
121 YGSSYEDYWGOGTTLTVSS 139
1 YGSSYEDYWGOGTTLTVSS 139

Qy
118 -AATMDYWGOGTTLTVSS 135
1 -AATMDYWGOGTTLTVSS 135

RESULT 12
ENTRY PL0208 #type fragment
TITLE Ig heavy chain precursor V region anti-idiotypic antibody
ORGANISM E225 mouse (strain BALB/c) (fragment)
#formal_name Mus musculus #common_name house mouse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998

ACCESSIONS
REFERENCE PL0208
#authors Soucoun, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.U.
#journal Mol. Immunol. (1990) 27:429-433
#title Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacting with a private idiotope of the anti-lysozyme D1.3 antibody.
#cross-references M01D:90309764

CLASSIFICATION
#molecule_type mRNA
#accession PL0208
#residues 1-136 ##label SOU
#experimental_source hybridoma cell E225
FEATURE
##superfamily immunoglobulin V region; immunoglobulin homology
1-19 #domain signal sequence #status predicted #label SIG\
34-117 #domain immunoglobulin homology #label IMM\
50-54 #region complementarity-determining 1\
69-85 #region complementarity-determining 2\
118-125 #region complementarity-determining 3\
118-121 #region D region\
122-136 #region JH region
#length 136 #checksum 9740

Query Match
Best Local Similarity 67.9%; Score 678; DB 2; Length 136;
Matches 91; Conservative 26; Mismatches 18; Indels 1; Gaps 1;

Db
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Qy
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Db
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Qy
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Db
121 YGSSYEDYWGOGTTLTVSS 136
1 YGSSYEDYWGOGTTLTVSS 136

Qy
120 YGSSYEDYWGOGTTLTVSS 135
1 YGSSYEDYWGOGTTLTVSS 135

RESULT 13
ENTRY S31600 #type fragment
TITLE Ig heavy chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

ACCESSIONS
REFERENCE S31600
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelier, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver.
#accession S31600 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-136 ##label CUI
#cross-references EMBL:Z4165; NID:g30994; PIDN:CAA78534.1; PID:g30995

CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
34-117 #domain immunoglobulin homology #label IMM
#length 136 #checksum 9862

SUMMARY

Query Match
Best Local Similarity 71.3%; Pred. No. 1.81e-100;
Matches 97; Conservative 12; Mismatches 25; Indels 2; Gaps 2;

Db
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Qy
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60
1 MGNMCIIFLVATATGVSQVQLVDSGAEVKKPKSSSVKVCASGYTFDYAIQWVRAAP 60

Db
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Qy
61 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120
1 GAGLEWIGHIDPNSGCTKNEFKKATLTVDKPSSTAYMWSLSEDSAVYCAR 120

Db
121 AF-DINGGCTMYTVSS 135
1 AF-DINGGCTMYTVSS 135

Qy
120 WYMDYWGOGTTLTVSS 135
1 WYMDYWGOGTTLTVSS 135

RESULT 14
ENTRY F29380 #type fragment
TITLE Ig heavy chain precursor V region (A003 40/567) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

ACCESSIONS
REFERENCE F29380
#authors Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
#journal J. Biol. Chem. (1987) 262:113579-113583
#title Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances.
#cross-references M01D:88007582
#accession F29380
#molecule_type mRNA
#residues 1-137 ##label CHE
#cross-references GB:M17165; GB:J02815; NID:g195409; PIDN:AAA38294.1; PID:g195410

	CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homologous heterotetramer; immunoglobulin
KEYWORDS		
FEATURE		
34-117		
SUMMARY	#domain immunoglobulin homology #label IMM	
	#length 137 #checksum 1052	
Query Match	67.5% Score 674; DB 2; Length 137;	
Best Local Similarity	66.6%; Pred. NO.4.29e+100;	
Matches	96; Conservative 20; Mismatches 18; Indels 4; Gaps 3;	
Dd	1 MGWNIILFLVATPTGVSHQVOYQOAGAEIYPKSTIVKLSCASGYNFTYYINWKLRP 60 ::: :::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: 1 MGWNIIIFLVTATTGVSQVOLVGSAEVRKKSGSVKTKCASGETITFDALIQWRAP 60	
Oy	61 GGGLSEMGIDIPGSGSTNYNEKRKAATLTVDTSSTAAYMQLSLASEDSALLYCAROVG 120 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : 61 GGGLSEMGIWINIIDNTNNNQKFRAKTMTVDKSTSTAYNELSLSRSEDYAVYCARA--A 118 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Dd	121 ETVF-AWGOGTLTVA 137 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Oy	119 -AWMYDYGOGTLTVTSS 135	
RESULT 15		
ENTRY	T01407	#type fragment
TITLE	Ig heavy chain (mouse M104e) - mouse (fragment)	
ORGANISM	Homo sapiens Mus sp.	#common_name mouse
DATE	20-Sep-1999	#sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
ACCESSIONS	T01407	
REFERENCE	T14317	
AUTHORS	Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Blom, S.; Onishi, S.; Yamamoto, Y.; Yamamoto, H.; Fujimoto, S. Microbiol. Immunol. (1992) 36:855-863 Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and anti-idiotypic antibodies involved in B-B cellular interaction.	
#journal	Molecular Immunol. (1992) 36:855-863	
#title	Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and anti-idiotypic antibodies involved in B-B cellular interaction.	
#cross-references	MIMD:93116538	
#accession	T01407	
#status	translated from GB/EMBL/DDBJ	
molecule_type	mRNA	
#residues	1-140	#label TAK
GENTICS	#cross-references EMBL:S1851; NID:g26z657; PID:e69004	
gene	M104e myeloma immunoglobulin heavy chain	
SUMMARY	#length 140 #checksum 7020	
Query Match	67.1% Score 670; DB 2; Length 140;	
Best Local Similarity	66.9%; Pred. NO.2.40e+99;	
Matches	91; Conservative 22; Mismatches 22; Indels 1; Gaps 1;	
Dd	1 MGWSMIFFLLSGTAGVLSEYOLOQSOPELVKRGASVSKSRASGTETDYMKWVKOSH 60 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : 1 MGWNIIIFLVTATTGVSQVOLVGSAEVRKKSGSVKTKCASGETITFDALIQWRAP 60	
Oy	61 GKSIEMIGDIIPNNNGISTYNOKRKGAATLTVDKSSTAAYMLNSLTSDSAVYTCAARD 120 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : 61 GGGLSEMGIDIPNNNGISVINIIDNTNNNQKFRAKTMTVDKSTSTAYNELSLSRSEDYAVYCARA-A 119	
Dd	121 WYPDWAGCTTYVSS 136 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :	
Oy	120 WYMDYWGGTLTVTSS 135	

Search completed: Mon Aug 7 18:59:45 2000
Job time : 14 secs.


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OY 61 GCGLEWIGVINTYDNTNKNQKFKGKATMTVDKSTFAYMELSLRSEDYAVYYCARA-A 119
Db 121 NYEDYWGOGTTLTVSS 136
OY 120 WYMDYWGOGTTLTVSS 135

RESULT 2
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81234548.
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.; variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL: J00539; AAA38172.1; -
DR PIR: A02038; G2MS43.
DR PIR: PF00047; Ig; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MM; ADD5681BF44B8EC9 CRC64;

Query Match 68.4%; Score 683; DB 1; Length 137;
Best Local Similarity 67.2%; Pred. No. 1.15e-155;
Matches 92; Conservative 23; Mismatches 20; Indels 2; Gaps 1;

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AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6;
RX MEDLINE: 81234548.
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL: J00529; AAA38170.1; -
DR PIR: A02034; MEMS18.
DR PIR: PF00047; Ig; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MM; 1B57DDAFDC9F465 CRC64;

Query Match 68.0%; Score 679; DB 1; Length 139;
Best Local Similarity 68.3%; Pred. No. 1.12e-134;
Matches 95; Conservative 24; Mismatches 16; Indels 4; Gaps 1;

```

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 84248078.
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.:
 RT "Illegitimate recombination generates a class switch from C mu to C
 delta in an iD-secreting plasmacytoma."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
 DR PIR: A02033; HVM57.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL
 FT CHAIN 1 20
 FT DOMAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
 FT DOMAIN 50 54 FRAMEWORK 1.
 FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 69 85 FRAMEWORK 2.
 FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 118 127 FRAMEWORK 3.
 FT DOMAIN 128 138 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 41 115
 FT NON_TER 138 138 BY SIMILARITY.
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
 Query Match 66.7%; Score 666; DB 1; Length 138;
 Best Local Similarity 68.1%; Pred. No. 1,84e-131;
 Matches 94; Conservative 20; Mismatches 21; Indels 3; Gaps 2;
 Db 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTSYMMHWKORP 60
 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 QY 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 Db 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCA 120
 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCARA-A 119
 QY 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCARA-A 119
 Db 121 YDWEYVWOGGTLVPEFA 138
 120 WY--MDYWGOGTLVTVSS 135
 QY 120 WY--MDYWGOGTLVTVSS 135
 RESULT 5
 ID HV05_MOUSE STANDARD; PRT; 117 AA.
 AC P01749;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.:
 RT "Heavy chain variable region contribution to the NPb family of
 antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637 (1981).
 CC -I- MISCELLANEOUS; THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 CC PIR: A02033; HVM52.
 DR PIR: A02033; HVM52.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL
 FT CHAIN 1 19
 FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115
 FT NON_TER 117 115 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 66.0%; Score 659; DB 1; Length 117;
 Best Local Similarity 76.7%; Pred. No. 9.87e-130;
 Matches 89; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
 Db 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTSYMMHWKORP 60
 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 QY 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 Db 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCA 116
 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCARA 116
 QY 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCARA 116
 RESULT 6
 ID HV05_MOUSE STANDARD; PRT; 117 AA.
 AC P01749;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.:
 RT "Heavy chain variable region contribution to the NPb family of
 antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637 (1981).
 CC -I- MISCELLANEOUS; THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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 CC -----
 CC EMBL: J00536; AAA38605.1; -
 CC PIR: A02031; HVM53.
 DR PIR: A02031; HVM53.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL
 FT CHAIN 1 19
 FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 3.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115
 FT NON_TER 117 115 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;
 Query Match 64.7%; Score 646; DB 1; Length 117;
 Best Local Similarity 75.2%; Pred. No. 1.59e-126;
 Matches 88; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
 Db 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTSYMMHWKORP 60
 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 QY 1 MGNWCIIFLVATATDVSHVSOVLOQPGAEVLRPGASVQSCSKASGTFPTDYAIOWKORP 60
 Db 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCA 117
 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCAR 117
 QY 61 GGGLEWIGINIPYSDSTHYNOKFKKATLTVDKSSSTAYMOJSLTSEDSAYVYCAR 117

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RESULT 7
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE: 8252818.
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.,
RT "Somatic mutation in genes for the variable portion of the
RT Immunoglobulin heavy chain."
RL Science 216:309-311(1982).
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CC -----
DR EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HVM5G7.
DR PIR: P00047; 19; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 20 140
FT SEQUENCE 140 AA; 15514 MW; 254ACBBE31DA5CE8 CRC64;
SQ
Query Match 63.8%; Score 637; DB 1; Length 140;
Best Local Similarity 65.7%; Pred. No. 2.63e-124;
Matches 92; Conservative 24; Mismatches 19; Indels 5; Gaps 2;
Db 1 MGMSIFLFLVYAGVHSEVQLQSGAEVLRAGSVKMSCKASGYFTSYGMVKORP 60
1 MGWNCIFFLVTTATGVHSGVQLVQSGAEVKKPKSSVKASGYFTDYAIQWVQAP 60
QY
Db 61 GGGLEWIGINPVGNGYINYEKFKGKTLTYDKSSSTAYMOJRLTSEDSAVYCARSHY 120
61 GGGLEWIGVINIYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDTAVYCARA-- 118
QY
Db 121 YGSGYDFDYGGGTPLTVSS 140
119 --AWY-MDYMGQGLTVYSS 135
QY
RESULT 8
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE: 8134548.
RA Bothwell A.L.M., Pasikind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.,
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
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RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: A02030; HVM523.1.
DR PIR: P00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V REGION 23.
FT NON_TER 20 147
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;
Query Match 63.1%; Score 630; DB 1; Length 117;
Best Local Similarity 71.8%; Pred. No. 1.39e-122;
Matches 84; Conservative 18; Mismatches 15; Indels 0; Gaps 0;
Db 1 MGMSCTFLVVAANGVHSGVQLQPGTELVKPGASVYKLSCKASGYFTSYGMHVKORP 60
1 MGWNCIFFLVTTATGVHSGVQLVQSGAEVKKPKSSVKASGYFTDYAIQWVQAP 60
QY
Db 61 GGGLEWIGINPVGNGYINYEKFKGKTLTYDKSSSTAYMOJRLTSEDSAVYCAR 117
61 GGGLEWIGVINIYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDTAVYCAR 117
QY
RESULT 9
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88296408.
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,
RA Ono H., Fukuhara S., Honjo T.,
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X07448; -. NOT_ANNOTATED_CDS.
DR PIR: S00476; HVH035.
DR PIR: P00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 20 117
FT SEQUENCE 117 AA; 13009 MW; BE61CEB3F8CE97BD CRC64;
SQ
Query Match 62.7%; Score 626; DB 1; Length 117;
Best Local Similarity 73.5%; Pred. No. 1.35e-121;
Matches 86; Conservative 9; Mismatches 22; Indels 0; Gaps 0;
Db 1 MDWTWRLFLVAAGVHSGVQLVQSGAEVKKPKGASVYKSCASGYFTSYGMHVKORP 60
1 MGWNCIFFLVTTATGVHSGVQLVQSGAEVKKPKSSVKASGYFTDYAIQWVQAP 60
QY
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Db 61 GGGLEMMGRINPNSGGTNYAKFOGRTVSTDRPISSTAYMELSLRSEDPAVYYCAR 117
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
OY 61 GGGLEMMIGVINITYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117

RESULT 10
ID HV49_MOUSE STANDARD: PRT: 117 AA.
AC P06328:
DT 01-JUN-1988 (Rel. 06, Created)
DT 01-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85099340.
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
    unrearranged VH gene segments."
    Cell 40:271-281(1983).
RL -----
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    or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: M13788; AAA8506.1; -
DR PIR: A03035; MHMSB4.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12834 MW: 88622FAC67ABD345 CRC64;

Query Match
Best Local Similarity 62.5%; Score 624; DB 1; Length 117;
Matches 81; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

Db 1 MGSCIMLFLAATATGYHSPVOLOQPGAEVLKPGASVKLSCKSGYFTSYMHMVKORP 60
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
OY 1 MGNCNIIFFLVATATGHSOVLOVSGAEVKKPGSSVKSCASGYFTFYAIDQWQAP 60
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
Db 61 GGGLEMMIGVINITYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
OY 61 GGGLEMMIGVINITYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||

RESULT 11
ID HV1B_HUMAN STANDARD: PRT: 117 AA.
AC P01743:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83144028.

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RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
    (VH) gene subgroups."
    Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
RL -----
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    or send an email to license@isb-sdb.ch).
CC -----
DR EMBL: J00240; AAA5298.1; -
DR PIR: A02024; HYH09.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12946 MW: 2D3F92FC60CD1FE7 CRC64;

Query Match
Best Local Similarity 72.6%; Score 623; DB 1; Length 117;
Matches 85; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Db 1 MDNTWRFCLAVAPRAHSGVLOVSGAEVKKPGASVKSCASGYFTFNYHMWRQAP 60
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
OY 1 MGNCNIIFFLVATATGHSOVLOVSGAEVKKPGSSVKSCASGYFTFYAIDQWQAP 60
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
Db 61 GGGLEMMIGVINITYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||
OY 61 GGGLEMMIGVINITYDNTNINQKFKGKATMTVDKSTAYMELSLRSEDPAVYYCAR 117
    |||||:| 11 ||| 11:| 11 ||||| 11:| 11 |||||

RESULT 12
ID HV09_MOUSE STANDARD: PRT: 117 AA.
AC P01753; P11271.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE: 81234548.
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NBP family of
    antibodies: somatic mutation evident in a gamma 2a variable region."
    Cell 24:625-637(1981).
RL -----
CC -1- RELATED GENES: THIS GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
DR PIR: B02034; HYMS61.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12890 MW: 16191A08CB17F5A CRC64;

Query Match
Best Local Similarity 70.1%; Score 622; DB 1; Length 117;
Matches 82; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

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Sun Aug 27 09:11:04 2000

US-09-249-011-6.rsp

Page 7

[illegible]

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Search completed: Mon Aug 7 18:58:33 2000
Job time : 9 secs.
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 WISE (TM)

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Merch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 7 18:58:52 2000; Maspar time 18.21 Seconds
 513.907 Million cell updates/sec

Tabular output not generated.

Title: >US-09-249-011-6
 Description: (1-135) from US09249011.pep
 Perfect score: 999
 Sequence: 1 MGWNCIFFLVTATGVHSQ.....ARAWMDYMGQGLVTYSS 135

Scoring table: PAM 150
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptrembl12
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 41.383; Variance 68.903; scale 0.601
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	61.7	61.8	150	4	Q9Y298	IGG VH PROTEIN PRECURS	1.36e-118
2	58.9	58.9	157	4	Q9Y298	VH1 PROTEIN PRECURSOR	1.59e-111
3	53.9	54.0	118	11	Q9Z1C4	ANTI-PORCINE YCAM MAB	1.21e-99
4	53.2	53.3	117	11	Q9Z1C6	ANTI-PORCINE YCAM MAB	5.96e-98
5	41.0	41.0	147	4	Q9Y509	VH3 PROTEIN (FRAGMENT)	8.11e-69
6	34.7	34.7	150	4	Q9Y573	VH4 HEAVY CHAIN VARIANT	4.19e-54
7	30.0	30.0	76	4	Q9Y742	IG HEAVY CHAIN VARIANT	2.41e-43
8	27.1	27.1	82	4	Q9Y729	IG HEAVY CHAIN VARIANT	7.95e-37
9	26.8	26.8	77	4	Q9Y726	IG HEAVY CHAIN VARIANT	3.70e-36
10	26.7	26.7	77	4	Q9Y726	IG HEAVY CHAIN VARIANT	6.18e-36
11	26.6	26.6	81	4	Q9Y721	IG HEAVY CHAIN VARIANT	1.02e-35
12	26.4	26.4	79	4	Q9Y731	IG HEAVY CHAIN VARIANT	2.86e-35
13	26.4	26.4	88	4	Q9Y737	IG HEAVY CHAIN VARIANT	2.86e-35
14	26.0	26.0	82	4	Q9Y732	IG HEAVY CHAIN VARIANT	2.20e-34
15	25.4	25.4	72	4	Q9Y738	IG HEAVY CHAIN VARIANT	4.66e-33
16	25.3	25.3	81	4	Q9Y734	IG HEAVY CHAIN VARIANT	7.74e-33
17	25.2	25.2	78	4	Q9Y723	IG HEAVY CHAIN VARIANT	1.28e-32
18	25.2	25.2	81	4	Q9Y719	IG HEAVY CHAIN VARIANT	1.28e-32
19	25.1	25.1	78	4	Q9Y730	IG HEAVY CHAIN VARIANT	2.13e-32
20	25.0	25.0	76	4	Q9Y733	IG HEAVY CHAIN VARIANT	3.54e-32

ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	150 AA.
AC	Q9Y298:			
DT	01-NOV-1999 (TREMblrel. 12, Created)			
DT	01-NOV-1999 (TREMblrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)			
DE	IGG VH PROTEIN PRECURSOR (FRAGMENT).			
GN	IGG VH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 98322155.			
RA	JACQUEMIN M.G., VANDER ELST L.P.L.;			
RT	"Mechanism and kinetics of factor VIII inactivation: study with an			
RT	IgG monoclonal antibody derived from a hemophilia A patient with			
RT	inhibitor."			
RL	Blood 92:496-506(1998).			
DR	EMBL; AJ224083; CAA11829.1; -.			
KW	Signal.			
FT	SIGNAL.			
FT	NON_TER			
SQ	SEQUENCE	150 AA; 16031 MW; B18EC39A CRC32;		
Query Match	61.8%; Score 617; DB 4; Length 150;			
Best Local Similarity	63.2%; Pred. No. 1.36e-118;			
Matches	86; Conservative 19; Mismatches 30; Indels 1; Gaps 1;			
Db	1 MDMTRILEFLVAANGTHAOLVQSGAEVKRPGASVYSCVSYTLTLEPVHWVGAP 60			
QY	1 MGWNCIFFLVTATGVHSQVQVQSGAEVKKRPGASVYSCASITFTDVAIQWRAP 60			
QY	61 GGLGLENVGSFDESGSITAREFGSVTMTADTSDIAYMELSSIRSDTFAVYCAVPDP 120			
Db	121 DAFDMGQGTLYTVSS 136			
QY	120 WTMDYMGQGLTVTVSS 135			
RESULT 2				
ID	Q9Y578	PRELIMINARY:	PRT:	157 AA.

AC 095976;
DB 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last annotation update)
DE VHL PROTEIN PRECURSOR (FRAGMENT).
GN VHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RA JOX A., ZANDER T., KUEPPERS R., IRSCH J., KANZLER H., KORNACKER M.,
BOHLEN H., DIEHL V., WOLF J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
patient with mixed cellularly Hodgkin's disease is associated with
somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ005570; CA06599.1; -
KM Signal.
FT SIGNAL. 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 88468024 CRC32;
Query Match 58.9%; Score 588; DB 4; Length 157;
Best Local Similarity 60.0%; Pred. No. 1,59e-111;
Matches 84; Conservative 19; Mismatches 32; Indels 5; Gaps 2;
DB 1 MDMTRECLLAAPVAGVSOVLVOSGAELKRPAGSVKCTGYFTSYIHVROPR 60
1 MGNMCIFFLTATGVSQVLVOSGAELKRPAGSVKCTGYFTSYIHVROPR 60
QY 1 MGNMCIFFLTATGVSQVLVOSGAELKRPAGSVKCTGYFTSYIHVROPR 60
DB 61 GGGLEHMGIGCPGVSTMCARKEPGRILMTNTSTTYVMELSLREDTAVYICARAA- 119
61 GGGLEHMGIGCPGVSTMCARKEPGRILMTNTSTTYVMELSLREDTAVYICARAA- 119
QY 61 GGGLEHMGIGCPGVSTMCARKEPGRILMTNTSTTYVMELSLREDTAVYICARAA- 119
DB 121 WRSNGNHMGOGTPTVYSS 140
121 WRSNGNHMGOGTPTVYSS 140
QY 120 W----YMDYMGOGTPTVYSS 135
RESULT 3
ID 0921C4 PRELIMINARY; PRT; 118 AA.
AC 0921C4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last annotation update)
DE ANTI-PORCINE VCA-MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA MOELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SQUINTO S.P.,
MATIS L.M., EVANS M.J.;
RT "Humanized porcine VCA-M-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78801; AAD00293.1; -
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13036 MW; 45653221 CRC32;
Query Match 54.0%; Score 539; DB 11; Length 118;
Best Local Similarity 66.9%; Pred. No. 1,21e-99;
Matches 79; Conservative 17; Mismatches 20; Indels 2; Gaps 2;
DB 1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60
1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60
QY 1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60

DB 61 TOKRGKATLADKSSSTAYMOLSLASEDSAVYICARRVGGYFDYMGOTLVYSS 118
80 NOKFKGKATMTVSKSTAYMELSLRSEDYAVYICAR-A-AMTMDYMGOGTPTVYSS 135
QY 80 NOKFKGKATMTVSKSTAYMELSLRSEDYAVYICAR-A-AMTMDYMGOGTPTVYSS 135
RESULT 4
ID 0921C6 PRELIMINARY; PRT; 117 AA.
AC 0921C6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last annotation update)
DE ANTI-PORCINE VCA-MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA MOELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SQUINTO S.P.,
MATIS L.M., EVANS M.J.;
RT "Humanized porcine VCA-M-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78799; AAD00291.1; -
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13122 MW; DC234181 CRC32;
Query Match 53.3%; Score 532; DB 11; Length 117;
Best Local Similarity 59.3%; Pred. No. 5,96e-98;
Matches 70; Conservative 28; Mismatches 17; Indels 3; Gaps 2;
DB 1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60
1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60
QY 1 QVOVOSGAEVKKRPGSSVSKASGYFTFYAIOVWROAPGGLWIGVINYNTNY 60
DB 61 NORLKDAILTVDKSSMTAVMOFSGPTSEDSAVYICTRGVSWE-AVWGOGTPTVYSS 117
61 NORLKDAILTVDKSSMTAVMOFSGPTSEDSAVYICTRGVSWE-AVWGOGTPTVYSS 117
QY 61 NORLKDAILTVDKSSMTAVMOFSGPTSEDSAVYICTRGVSWE-AVWGOGTPTVYSS 117
DB 80 NOKFKGKATMTVSKSTAYMELSLRSEDYAVYICAR-A-AMTMDYMGOGTPTVYSS 135
80 NOKFKGKATMTVSKSTAYMELSLRSEDYAVYICAR-A-AMTMDYMGOGTPTVYSS 135
QY 80 NOKFKGKATMTVSKSTAYMELSLRSEDYAVYICAR-A-AMTMDYMGOGTPTVYSS 135
RESULT 5
ID 09Y509 PRELIMINARY; PRT; 147 AA.
AC 09Y509;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, last annotation update)
DE VHL PROTEIN (FRAGMENT).
GN VHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 96071149.
RA CAO J., VESICIO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
LICHENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -
FT NON_TER 1 1
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;
Query Match 41.0%; Score 410; DB 4; Length 147;
Best Local Similarity 50.5%; Pred. No. 8,11e-69;
Matches 53; Conservative 27; Mismatches 23; Indels 2; Gaps 2;
DB 1 QVHLVSGGAVOPGSLRSCASGFTSTYMSVNRQAPGGLWVALIS-YDGSIOY 59
1 QVHLVSGGAVOPGSLRSCASGFTSTYMSVNRQAPGGLWVALIS-YDGSIOY 59
QY 1 QVHLVSGGAVOPGSLRSCASGFTSTYMSVNRQAPGGLWVALIS-YDGSIOY 59

Best Local Similarity 42.9%; Pred. No. 3,70e-36;
Matches 33; Conservative 22; Mismatches 20; Indels 2; Gaps 1;

Db 1 YWMNWRQAPGCELOWSVTTEGCVTFPPDSYKGRFSISRDNSRNTLYLQNSLSRAEDT 60

QY 51 YAIOWWRQAPGGGLEWIGVINIYDNTNYNQKFKRATMTVDKSTAYWELSLRSED 110

Db 61 AATYCARGRKSEGGDYK 77

QY 111 AVYYCARAAAY--MDY 125

RESULT 10 PRELIMINARY: PRT: 77 AA.

ID 075726: PRELIMINARY: PRT: 77 AA.

AC 075726: PRELIMINARY: PRT: 77 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC [1]

RP SEQUENCE FROM N.A.

RC TISSUE-INTESINE:

RA FISCHER M., KUEPPERS R.;

RT "Human Iga and Igm secreting intestinal plasma cells carry heavily

mutated VH region genes.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ009523; CA08730.1; -

DR HSSP: P01772; 2IG2.

FT NON_TER 1 77 1

FT NON_TER 1 77 1

SQ SEQUENCE 77 AA: 9022 MW: EB7B458D CRC32:

Query Match 26.7%; Score 267; DB 4; Length 77;

Best Local Similarity 45.5%; Pred. No. 6.18e-36;

Matches 35; Conservative 18; Mismatches 22; Indels 2; Gaps 1;

Db 1 YELTWROAPGKLEWVATINEDGKRYVDSYKGRFTISRDNATSLYQNSLSRAEDT 60

QY 51 YAIOWWRQAPGGGLEWIGVINIYDNTNYNQKFKRATMTVDKSTAYWELSLRSED 110

Db 61 AATYCARGRKSEGGDYK 77

QY 111 AVYYCARAAAY--MDY 125

RESULT 11 PRELIMINARY: PRT: 81 AA.

ID 075721: PRELIMINARY: PRT: 81 AA.

AC 075721: PRELIMINARY: PRT: 81 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH.

Query Match 26.6%; Score 266; DB 4; Length 81;

Best Local Similarity 46.3%; Pred. No. 1.03e-35;

Matches 31; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

Db 2 YSMNWRQAPGKLEWVSLIGTDRATFYASSVGRFTISRDNATSLYQNSLSRAEDT 61

QY 51 YAIOWWRQAPGGGLEWIGVINIYDNTNYNQKFKRATMTVDKSTAYWELSLRSED 110

Db 62 AATYCAR 68

QY 111 AVYYCAR 117

RESULT 12 PRELIMINARY: PRT: 79 AA.

ID 075731: PRELIMINARY: PRT: 79 AA.

AC 075731: PRELIMINARY: PRT: 79 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

VH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC [1]

RP SEQUENCE FROM N.A.

RC TISSUE-INTESINE:

RA FISCHER M., KUEPPERS R.;

RT "Human Iga and Igm secreting intestinal plasma cells carry heavily

mutated VH region genes.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ009528; CA08735.1; -

DR HSSP: P01772; 2IG2.

FT NON_TER 1 79 1

FT NON_TER 1 79 1

SQ SEQUENCE 79 AA: 8842 MW: 7C40774F CRC32:

Query Match 26.4%; Score 264; DB 4; Length 79;

Best Local Similarity 41.3%; Pred. No. 2.86e-35;

Matches 31; Conservative 23; Mismatches 19; Indels 2; Gaps 2;

Db 1 GMTWROAPGKLEWVSIYSAAGSIHYAKSVGRFTISRDNATSLYQNSLSRAEDT 60

QY 52 AAIOWWRQAPGGGLEWIGVINIYDNTNYNQKFKRATMTVDKSTAYWELSLRSED 111

Db 61 VYTCARVGNKGLGY 75

QY 112 VYTCARA-A-WYMDY 124

RESULT 13 PRELIMINARY: PRT: 88 AA.

ID 075737: PRELIMINARY: PRT: 88 AA.

AC 075737: PRELIMINARY: PRT: 88 AA.

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)

Search completed: Mon Aug 7 18:59:13 2000
Job time : 21 secs.

 MWSEKEH
 (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Aug 7 19:00:01 2000; MasPar time 10.25 Seconds
 Tabular output not generated. 312.013 Million cell updates/sec

Title: >US-09-249-011-6
 Description: (1-135) from US09249011.pep
 Perfect Score: 999
 Sequence: 1 MGNMCIFFLVLTATGVHSQ.....ARAAHYNDYMGQGLVTVSS 135

Scoring table:
 PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 1:geneseqp

Statistics: Mean 30.791; Variance 156.235; scale 0.197

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
1	785	78.7	588	Anti-human Fas humanis	9.69e-54
2	772	77.3	140	DRG-200 Humanized ant	1.40e-52
3	770	77.1	470	Anti-Fas humanized ant	2.04e-52
4	759	76.0	588	Anti-human Fas humanis	1.66e-51
5	755	75.6	145	Anti-Fas humanized ant	3.56e-51
6	755	75.6	470	Anti-Fas humanized ant	3.56e-51
7	753	75.4	135	Humanised anti-Fac ant	5.21e-51
8	753	75.4	136	Sequence of the heavy	5.21e-51
9	750	75.1	163	Murine anti-ICAM monoc	9.22e-51
10	750	75.1	163	R6-5-D6 anti-ICAM-1 he	1.35e-50
11	748	74.9	135	Anti-Fac heavy chain v	1.63e-50
12	747	74.8	135	Anti-Fac heavy chain v	1.63e-50
13	745	74.6	135	Anti-Fac heavy chain v	1.63e-50
14	745	74.6	136	Anti-Fac heavy chain v	1.63e-50
15	737	73.8	133	Humc3 VH region.	2.39e-50
16	737	73.8	133	E-selectin CDR-grafted	1.09e-49
17	737	73.8	134	Variable region of mur	1.09e-49
18	721	72.2	140	Humanised heavy chain	2.30e-48
19	719	72.0	140	Humanised heavy chain	3.36e-48
20	718	71.9	180	Humanised heavy chain	4.06e-48
21	717	71.8	140	Heavy chain of a human	4.91e-48
22	709	71.0	136	Humanised heavy chain	2.25e-47
23	709	71.0	136	Chimeric anti-hepatiti	2.25e-47

24	709	71.0	136	1	W16340	Mouse-human chimaeric	2.25e-47
25	709	71.0	136	1 <td>W10584</td> <td>Anti-hepatitis B heavy</td> <td>2.25e-47</td>	W10584	Anti-hepatitis B heavy	2.25e-47
26	709	71.0	136	1 <td>W47517</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	W47517	Human anti-hepatitis a	2.25e-47
27	709	71.0	136	1 <td>W47510</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	W47510	Human anti-hepatitis a	2.25e-47
28	709	71.0	136	1 <td>P70624</td> <td>Sequence encoded by an</td> <td>2.25e-47</td>	P70624	Sequence encoded by an	2.25e-47
29	709	71.0	136	1 <td>W41054</td> <td>Human anti-hepatitis a</td> <td>2.25e-47</td>	W41054	Human anti-hepatitis a	2.25e-47
30	709	71.0	144	1 <td>W73187</td> <td>Fragment of gangliosid</td> <td>2.25e-47</td>	W73187	Fragment of gangliosid	2.25e-47
31	707	70.8	139	1 <td>W29753</td> <td>CDR-grafted humanised</td> <td>3.28e-47</td>	W29753	CDR-grafted humanised	3.28e-47
32	707	70.8	139	1 <td>R33953</td> <td>gH variable domain.</td> <td>3.28e-47</td>	R33953	gH variable domain.	3.28e-47
33	707	70.8	140	1 <td>W21851</td> <td>Humanised heavy chain</td> <td>3.28e-47</td>	W21851	Humanised heavy chain	3.28e-47
34	705	70.6	140	1 <td>W53815</td> <td>Murine Act-1 heavy cha</td> <td>4.80e-47</td>	W53815	Murine Act-1 heavy cha	4.80e-47
35	703	70.4	139	1 <td>W62205</td> <td>Humanised anti-HM1.24</td> <td>7.02e-47</td>	W62205	Humanised anti-HM1.24	7.02e-47
36	703	70.4	139	1 <td>W65773</td> <td>Anti-human HM1.24 anti</td> <td>7.02e-47</td>	W65773	Anti-human HM1.24 anti	7.02e-47
37	703	70.4	140	1 <td>W77294</td> <td>HM1.24 antibody heavy</td> <td>7.02e-47</td>	W77294	HM1.24 antibody heavy	7.02e-47
38	703	70.4	144	1 <td>W73172</td> <td>Heavy chain of ganglio</td> <td>7.02e-47</td>	W73172	Heavy chain of ganglio	7.02e-47
39	702	70.3	139	1 <td>W62212</td> <td>Humanised anti-HM1.24</td> <td>8.49e-47</td>	W62212	Humanised anti-HM1.24	8.49e-47
40	702	70.3	144	1 <td>W73189</td> <td>Fragment of gangliosid</td> <td>8.49e-47</td>	W73189	Fragment of gangliosid	8.49e-47
41	699	70.0	136	1 <td>W1818</td> <td>Humanised mouse anti-h</td> <td>1.50e-46</td>	W1818	Humanised mouse anti-h	1.50e-46
42	699	70.0	136	1 <td>W60036</td> <td>Human antibody F919 he</td> <td>1.50e-46</td>	W60036	Human antibody F919 he	1.50e-46
43	699	70.0	139	1 <td>W62211</td> <td>Humanised anti-HM1.24</td> <td>1.50e-46</td>	W62211	Humanised anti-HM1.24	1.50e-46
44	697	69.8	135	1 <td>W60866</td> <td>Variable region of an</td> <td>2.19e-46</td>	W60866	Variable region of an	2.19e-46
45	697	69.8	590	1 <td>W31751</td> <td>H chain subunit of Fas</td> <td>2.19e-46</td>	W31751	H chain subunit of Fas	2.19e-46

ALIGNMENTS

RESULT	1	Location/Qualifiers
ID	W1880 standard; Protein; 588 AA.	
AC	W1880;	
DT	18-JAN-1999 (first entry)	
DE	Anti-human Fas humanised antibody CH11 heavy chain HmH.	
KM	Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;	
KW	autoimmune disease; rheumatoid arthritis; therapy; human;	
OS	Human antibody engineering.	
OS	Homo sapiens.	
OS	Synthetic.	
FH	Key	
FT	Peptide	1..19
FT	Protein	/label= Sig-peptide
FT		20..588
FT	Region	/label= Mat-protein
FT		50..54
FT		/label= CDR1
FT		/note= "Complementarity determining region 1 from CH11 heavy chain"
FT	Region	69..84
FT		/label= CDR2
FT		/note= "Complementarity determining region 2 from CH11 heavy chain"
FT	Region	118..124
FT		/label= CDR3
FT		/note= "Complementarity determining region 3 from CH11 heavy chain"
EP	866131-AZ.	
PD	23-SEP-1998.	
PD	20-MAR-1998; 302113.	
PR	21-MAR-1997; JP-067938.	
PA	(SANY) SANKYO CO LTD.	
PI	Haruyama H, Nakahara K, Serizawa N, Takahashi T,	
PI	Yonehara S;	
DR	WPI: 98-482965/42.	
DR	N-PSDB; V61363.	
PT	Production of anti-Fas protein humanised antibodies - for use in	
PT	inducing apoptosis on Fas expressing cells in the treatment of	
PT	autoimmune diseases, especially rheumatoid arthritis	
PS	Claim 21; Page 105-107; 187pp; English.	
CC	This is the amino acid sequence of a humanised anti-Fas antibody	
CC	CH11 heavy chain, designated HmH. HmH is based on the heavy	
CC	chain (see W1888) of murine anti-human Fas monoclonal antibody	
CC	CH11. The humanised sequence was designed following selection of	
CC	donor residues from CH11 to be grafted onto acceptor molecule	
CC	21.28/CL. 2 Heavy chain sequences (see W1880-81) have been	
CC	designed, and each can be used in combination with any of 4	

CC light chain sequences (see W71876-79) to provide novel, claimed
CC humanised CH1 IGM antibodies that lack a J chain. These humanised
CC anti-human Fas antibodies are capable of inducing apoptosis in cells
CC expressing Fas (e.g. synovocytes) and are useful in the treatment
CC of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are
CC vectors such as pMNH5-1 including the HmuH nucleotide sequence
CC (see V61363), and host cells such as Escherichia coli pMNH5-1
CC (FERM BP-5863).
SO Sequence 588 AA:

Query Match 78.7%; Score 786; DB 1; Length 588;
Best Local Similarity 77.8%; Pred. No. 9,69e-54;

Matches 105; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

DB 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKRPASVSKASAGTFTDYMMHWAP 60
QY 1 MGSMTFLFLSGTAGVHSEVOLVOSGAEVKRPASVSKASAGTFTDYMMHWAP 60
DB 61 GGGLEWIGYIIPYNGGTGNKFKATLTVDNSATAYMELSRSEDTAVYCARAW 120
QY 61 GGGLEWIGYIIPYNGGTGNKFKATLTVDNSATAYMELSRSEDTAVYCARAW 120
DB 121 AMDYWGQGLTVTVSS 135
QY 121 YMDYWGQGLTVTVSS 135

RESULT 2
ID R55556 standard; Protein: 140 AA.
AC R55556;

DE 16-NOV-1994 (first entry)
KW DREG-200 Humanized antibody heavy chain variable region.
KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;
KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
KW complementarity determining region; CDR; monoclonal antibody; MAb;
KW framework; light chain; heavy chain; variable domain;
KW monoclonal antibody; acceptor antibody Eu; transgenic animal.
OS Mus sp.; Homo sapiens.

FM Key Location/Qualifiers

FT peptide 1..19
FT /label= Sig_peptide

FT region 50..54
FT /label= CDR1

FT region 69..85
FT /label= CDR2

FT region 118..129
FT /label= CDR3

FM WO9412215-A.
PN 09-JUN-1994.
PD 30-NOV-1993; U11612.
PR 01-DEC-1993; US-983946.
PA (PROT-) PROTEIN DESIGN LABS INC.
PI Co MS;
DR MPI; 94-199974/24.

DR P-PSDB; 066702.

PT New humanised antibody specific for L-selectin - with murine CDR
PT and human framework regions, inhibits binding of neutrophils to
PT endothelial cells and useful for treating or preventing

PT Inflammation

PS Disclosure; Fig. 3B; 60pp; English.

CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
CC corresponding to those of mouse MAb DREG-200 and heavy and light
CC chain variable region frameworks of the human acceptor antibody Eu.

CC Nucleotide and aa sequences are provided for the DREG-200 light
CC (Q66699), R55553 and heavy (Q66700, R55554) chain variable regions
CC and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702,
CC R55556) chain variable regions. The humanized antibodies can be

CC produced economically in large quantities by expression in mammalian
CC cell culture or in transgenic animals.

SO Sequence 140 AA:

Query Match

77.3%; Score 772; DB 1; Length 140;

Best Local Similarity 78.6%; Pred. No. 1.40e-52;
Matches 110; Conservative 11; Mismatches 14; Indels 5; Gaps 2;

DB 1 MGSMTFLFLVATATGHSQVOLVOSGAEVKRPSSVSKASAGTFTDYMMHWAP 60
QY 1 MGSMTFLFLVATATGHSQVOLVOSGAEVKRPSSVSKASAGTFTDYMMHWAP 60
DB 61 GGGLEWIGYIIPYNGGTGNKFKGRVITSDSTNAYMELSRSEDTAVYCARAW 120
QY 61 GGGLEWIGYIIPYNGGTGNKFKGRVITSDSTNAYMELSRSEDTAVYCARAW 120
DB 121 GNYVRFPDWGQGLTVTVSS 140
QY 121 --YMDY--WGQGLTVTVSS 135

RESULT 3
ID W83037 standard; Protein: 470 AA.
AC W83037;

DE 15-MAR-1999 (first entry)
KW Anti-Fas humanised antibody HEF7A heavy chain.
KW HEF7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HEF7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
OS Homo sapiens.

FM Synthetic.

FM Key Location/Qualifiers

FT peptide 1..19
FT /label= Sig_peptide

FT protein 20..470
FT /label= Mat_protein

FT region 20..140
FT /label= Variable

FT region 141..464
FT /label= Constant

FT region 50..54
FT /label= CDR H1

FT region 69..84
FT /label= CDR H2

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

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FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

FT region 118..129
FT /label= CDR H3

Query Match 77.3%; Score 772; DB 1; Length 140;

PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.
 PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANY) SANKYO CO LTD.
 PI Aiko S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR N-PSDB: V70104.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Example 3; Page 207; 292pp; English.
 CC This is the amino acid sequence of the VD type humanised heavy
 CC chain variable region of murine anti-human Fas monoclonal antibody
 CC HEF7A. It was utilised in a claimed humanised HEF7A heavy chain
 CC (see V70079). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HEF7A (see
 CC W83033-37) are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. Humanised antibodies are used to evaluate, in animal models,
 CC treatments of diseases that involve Fas/Fas ligand interactions, and
 CC also to treat such diseases, including autoimmune disease (e.g.
 CC systemic lupus erythematosus, Hashimoto's disease, graft versus host
 CC disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 145 AA;
 Query Match 75.6%; Score 755; DB 1; Length 145;
 Best Local Similarity 78.6%; Pred. No. 3,56e-51;
 Matches 110; Conservative 12; Mismatches 13; Indels 5; Gaps 2;
 Db 1 MGMSIIIFLVATAGVHSQVQLVQSGAEVKKPGASVVSVCASGYTFTDVAIQWVQAP 60
 QY 1 MGWNCIIFFLVTTAGVHSQVQLVQSGAEVKKPGSSVVSVCASGYTFTDAIQWVQAP 60
 Db 61 GORLEWMEIGIPSDSYTYNOKFKGKATLVDTASATYAMELSRSRSDTAVYYCARND 120
 QY 61 GOGLEWIGVINYDNTNINOKFKGKATLVDTKSTAYMELSRSRSDTAVYYCARA-- 118
 Db 121 YSNMNYFDVWEGEGLVTYSS 140
 QY 119 -A-WYMDYWGCGTLVTYSS 135
 RESULT 6
 ID W83036 standard; Protein: 470 AA.
 AC W83036;
 DE 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HEF7A heavy chain.
 KW HEF7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HEF7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT 1..19
 FT Peptide /Label= Sig_peptide
 FT 20..470
 FT Protein

FT FT /Label= Mat_protein
 FT Region 20..140
 FT /Label= Variable
 FT Region 141..464
 FT /Label= Constant
 FT Region 50..54
 FT /Label= CDR_H1
 FT /note= "claim 9"
 FT Region 69..84
 FT /Label= CDR_H2
 FT /note= "claim 9"
 FT Region 118..129
 FT /Label= CDR_H3
 FT /note= "claim 9"
 FT Region
 FT Region
 PN A09859701-A.
 PD 08-OCT-1998.
 PF 30-MAR-1998; 059701.
 PR 08-OCT-1997; JP-276064.
 PR 01-APR-1997; JP-082953.
 PR 25-JUN-1997; JP-169088.
 PA (SANY) SANKYO CO LTD.
 PI Aiko S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I,
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 98-543440/47.
 DR N-PSDB: V70079.
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 PS Claim 22; Page 212-213; 292pp; English.
 CC This is the amino acid sequence of the VD type humanised heavy
 CC chain of murine anti-human Fas monoclonal antibody HEF7A. E. coli
 CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
 CC fragment of the humanised VD type HEF7A heavy chain and DNA
 CC encoding human IgG1 constant region (see V70079), and is deposited
 CC as FERM BP-6074 (claimed). The invention provides methods for
 CC producing humanised antibodies by culturing host cells. Humanised
 CC versions of HEF7A (see W83033-37), like native HEF7A, are capable
 CC of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to
 CC treat such diseases, including autoimmune disease (e.g. systemic
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 SQ Sequence 470 AA;
 Query Match 75.6%; Score 755; DB 1; Length 470;
 Best Local Similarity 78.6%; Pred. No. 3,56e-51;
 Matches 110; Conservative 12; Mismatches 13; Indels 5; Gaps 2;
 Db 1 MGMSIIIFLVATAGVHSQVQLVQSGAEVKKPGASVVSVCASGYTFTDVAIQWVQAP 60
 QY 1 MGWNCIIFFLVTTAGVHSQVQLVQSGAEVKKPGSSVVSVCASGYTFTDAIQWVQAP 60
 Db 61 GORLEWMEIGIPSDSYTYNOKFKGKATLVDTASATYAMELSRSRSDTAVYYCARND 120
 QY 61 GOGLEWIGVINYDNTNINOKFKGKATLVDTKSTAYMELSRSRSDTAVYYCARA-- 118
 Db 121 YSNMNYFDVWEGEGLVTYSS 140
 QY 119 -A-WYMDYWGCGTLVTYSS 135
 RESULT 7
 ID R24107 standard; Protein: 135 AA.
 AC R24107;

DT 25-NOV-1992 (first entry)
 DE Humanised anti-Tac antibody heavy chain.
 KM Immunoglobulin; T cell related diseases; leukaemia; autoimmune;
 KM IL-2 receptor; recombinant; diagnosis; therapy.
 OS Synthetic.
 FH Key
 FT peptide
 FT 1. 19
 FT /note- "signal peptide"
 FT 20. 135
 FT /note- "mature peptide"
 PD DD-296964-A.
 PD 19-DEC-1991.
 PD 17-JAN-1990; 337159.
 PR 17-JAN-1990; DD-337159.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Queen CL, Selick HE;
 DR WPI; 92-167794/21.
 DR N-PSDB; Q24790.
 PT New humanised antibody specific for interleukin-2 receptor - with
 PT complementarity determ. regions and framework from different
 PT immunoglobulin(s), is non immunogenic and used to treat T-cell
 PT mediated disorders
 PS Disclosure; Fig 3; 21pp; German.
 CC The sequence is that of the humanised anti-Tac antibody heavy chain
 CC which is used in the production of a human-type immunoglobulin (19)
 CC that reacts specifically with p55-Tac protein and/or inhibits binding
 CC of human interleukin-2 (IL-2) to its specific receptor. The three
 CC complementary determining regions and amino acids 27, 30, 48, 67,
 CC 68, 93, 95, 98, 107, 108, 109 and 111 of human antibody Eu have been
 CC replaced with the corresponding amino acids in the anti-Tac heavy chain
 CC antibody. This produces a humanised antibody which has the same
 CC affinity as anti-Tac for IL-2 receptors. The Ig may be used to treat
 CC humans with T-cell related diseases such as transplant rejection,
 CC T cell leukaemia, or autoimmune diseases such as diabetes or multiple
 CC sclerosis. See also R24103-R24108.
 SQ Sequence 135 AA;
 Query Match 75.4%; Score 753; DB 1; Length 135;
 Best Local Similarity 77.8%; Pred. No. 5.21e-51;
 Matches 105; Conservative 15; Mismatches 15; Indels 0; Gaps 0;
 Db 1 MGNMWIFLFLSLGAGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYLMHWKAP 60
 QY 1 MGNWCIFFLVTATGVSQVLQVQSGAEVKKPGSSVYKSCAKSGYFTDTAIAQWQAP 60
 Db 61 GQGLEWIGVNIPTSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDYAVYYCARGG 120
 QY 61 GQGLEWIGVNIPTSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDYAVYYCARGG 120
 Db 121 VFDPYWGQGLTYVSS 135
 QY 121 VFDPYWGQGLTYVSS 135
 QY 121 YMDYWGQGLTYVSS 135
 RESULT 8
 ID R59512 standard; Protein; 136 AA.
 AC R59512;
 DT 31-DEC-1994 (first entry)
 DE Sequence of the heavy chain variable region of the
 DE humanised NA-8 antibody including signal sequence.
 KM Humanised antibody; NA-8; human CD18; complementarity determining region;
 OS Synthetic.
 FH Key
 FT peptide
 FT 1. 19
 FT /label= leader
 FT 50. 54
 FT /label= CDRL
 FT 69. 85
 FT /label= CDR2
 FT 118. 127
 FT /label= CDR3
 FT 139. 163
 FT domain /label= constant
 PD W09116927-A.
 PD 14-NOV-1991.
 PD 29-APR-1991; U02942.
 PF 27-APR-1990; GB-009549.
 PA (CELL-) CELTECH LTD.
 PA (BOEH) BOEHRINGER INGELHEIM PHA.
 PI Abair JR, Ahtwal DS, Rothlein RA;
 DR WPI; 91-353533/48.
 DR N-PSDB; Q14802.
 PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
 PT murine antibody NA-8, prevent binding of neutrophils to

PT endothelial cells, useful for treating inflammation
 PS Example; Fig 3b; 50pp; English.
 CC The mouse antibody NA-8 binds to human CD18. CDNA's for the heavy
 CC chain and light chain variable domain genes of NA-8 were cloned
 CC using anchored PCR. The cDNA variable domain sequences and the
 CC deduced AA sequences are shown in Q66845/R59509 and Q66846/R59510.
 CC The antibody Eu was chosen to provide the framework sequence for
 CC the humanisation of NA-8. At each posn. the AA was chosen to be the
 CC same as in the Eu antibody unless that posn. was: 1) in a CDR; 11)
 CC the Eu AA was atypical whilst the NA-8 AA was typical for human
 CC antibodies in that posn.; 111) Immediately adjacent to a CDR; 1v)
 CC the AA was physically close to the CDR. In addition the AA from NA-8
 CC was chosen at light chain posn. 49 because it was at the light-
 CC heavy chain interface. Humanised NA-8a has the same light chain
 CC as humanised NA-8 but in the heavy chain the human Eu AAs were
 CC retained at posns 67, 68, 70 and 74 rather than being replaced by
 CC the murine NA-8 AAs. Humanised NA-8a was used to determine whether
 CC these AAs were imp. in maintaining binding affinity. For the
 CC construction of genes for the humanised antibodies, nucleotide
 CC sequences were selected that encode the protein sequences of the
 CC humanised heavy and light chains, including signal peptides,
 CC generally using codons found in the mouse sequence. The gene
 CC sequence also include splice donor signals and an XbaI site at
 CC each end (See Q66847/R59511 and Q66848/R59512).
 SQ Sequence 136 AA;
 Query Match 75.4%; Score 753; DB 1; Length 136;
 Best Local Similarity 75.7%; Pred. No. 5.21e-51;
 Matches 103; Conservative 19; Mismatches 13; Indels 1; Gaps 1;
 Db 1 MGNMWIFLFLSLGAGVHSGVOLVQSGAEVKKPGSSVYKSCAKSGYFTSTYLMHWKAP 60
 QY 1 MGNWCIFFLVTATGVSQVLQVQSGAEVKKPGSSVYKSCAKSGYFTDTAIAQWQAP 60
 Db 61 GQGLEWIGVNIPTSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDYAVYYCARGG 120
 QY 61 GQGLEWIGVNIPTSTGYEYNQKFKDRTTADSTNTAYNELSLRSEDYAVYYCARGG 120
 Db 121 VFDPYWGQGLTYVSS 136
 QY 121 VFDPYWGQGLTYVSS 136
 QY 121 YMDYWGQGLTYVSS 135
 RESULT 9
 ID R15060 standard; Protein; 163 AA.
 AC R15060;
 DT 13-FEB-1992 (first entry)
 DE Murine anti-ICAM monoclonal antibody heavy chain.
 KM Intercellular adhesion molecule; variable region; (VH); mouse;
 KM R5-5-D6 murine Mab; complementarity determining region; CDR.
 OS Mus musculus.
 FH Key
 FT peptide
 FT 1. 19
 FT /label= leader
 FT 50. 54
 FT /label= CDRL
 FT 69. 85
 FT /label= CDR2
 FT 118. 127
 FT /label= CDR3
 FT 139. 163
 FT domain /label= constant
 PD W09116927-A.
 PD 14-NOV-1991.
 PD 29-APR-1991; U02942.
 PF 27-APR-1990; GB-009549.
 PA (CELL-) CELTECH LTD.
 PA (BOEH) BOEHRINGER INGELHEIM PHA.
 PI Abair JR, Ahtwal DS, Rothlein RA;
 DR WPI; 91-353533/48.
 DR N-PSDB; Q14802.
 PT New humanised CDR-grafted anti-ICAM antibodies - used to treat
 PT and prevent inflammation (e.g. psoriasis) tumours, viral

PT Infections and asthma and in diagnosis
PS Disclosure: Fig 2: 83pp: English.
CC The heavy chain coding sequence was isolated from a cDNA library
CC prep'd. from hybridoma cell line R6-5-D6 which secretes murine
CC IgG2a/kappa antibody. The library was screened using a 980bp
CC BamHI-EcoRI fragment of a previously isolated mouse IgG2a constant
CC region clone. The murine framework-encoding sequences (i.e. not
CC encoding CDRs) will be replaced by human framework sequences to
CC produce recombinant (CDR-grafted humanised) antibody molecules
CC having specificity for ICAM-1.
SQ Sequence 163 AA;
Query Match 75.1%; Score 750; DB 1; Length 163;
Best Local Similarity 70.3%; Pred. No. 9,22e-51;
Matches 97; Conservative 25; Mismatches 13; Indels 3; Gaps 1;
Db 1 MGWSCIIFFLVATATGHSQVQLQSGPELVKPGYVKRISKSGSYTFDAIHVKESH 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDVAIQWVQAP 60
Db 61 AKSLMEIGVTSAGDTNRYNOKFKKATMTVDKSSNTAYLELRLTSDSAIYVCARGW 120
QY 61 GGGLEWIGVINYIDNTNRYNOKFKKATMTVDKSTSTAYMELSSLRSEDTAVYICARAAW 120
Db 121 LLSFDYWGQGTTLTVSS 138
QY 121 YM---DYWGQGTTLTVSS 135
RESULT 10
ID R15200 standard; Protein: 163 AA.
AC R15200;
DT 14-FEB-1992 (first entry)
DE R6-5-D6 anti-ICAM-1 heavy chain.
KW Intercellular adhesion molecule-1; antibody; chimaeric.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 1..19
FT /label= signal_sequence
FT region 50..54
FT /label= CDR
FT region 69..85
FT /label= CDR
FT region 118..127
FT /label= CDR
FT region 139..149
FT /label= CDR
FT region 150..163
FT /label= constant_domain
FN MO9116928-A.
PN 14-NOV-1991.
PD 29-APR-1991; 002846.
PR 27-APR-1990; GB-009548.
RA (CELL-) CELLTRECH LTD.
PA (BOHR) BOEHRINGER INGELHEIM PHA.
PI Adair JR, Robinson MK, Bright SM, Rothlein RA;
DR WPI: 91-353534/48.
DR N-PSDB: 014652.
PT New humanised chimeric anti-ICAM-1 antibodies - useful in
PT treating inflammation e.g. psoriasis and ulcerative colitis to
PT suppress metastasis of haematopoietic tumour cell and in
PT diagnosis.
PS Disclosure: Fig 2: 85pp: English.
CC The sequence comprises the signal sequence, variable region and part
CC of the constant region for the R6-5-D6 murine MAB heavy chain. The
CC hybridoma cell line R6-5-D6 producing the anti ICAM-1 Ab was provided
CC by Boehringer Ingelheim Pharmaceuticals Inc. The cells were grown
CC and mRNA isolated and used to prepare cDNA for a library in pSP64
CC vector DNA. The library was grown in E. coli LM1035 and colonies
CC screened using a probe complementary to a sequence in the mouse
CC kappa constant region or with a 980 bp BamHI-EcoRI restriction
CC fragment of a previously isolated mouse IgG2a constant region clone.
CC Tpn positive clones were isolated and rescreened. Positive clones

CC from the second round of screening were grown and the DNA inserts
CC sequenced. The protein sequence was deduced from the DNA. The DNA
CC was used to construct humanised Abs having chimeric variable regions,
CC esp. with IgG human constant region domains. The Abs can be used to
CC treat inflammation, to suppress metastasis of haematopoietic tumour
CC cells and growth of ICAM-1 expressing tumour cells, to treat viral
CC infection, to suppress extravascular migration of virally infected
CC leucocytes and to treat asthma.
CC See also R15199.
SQ Sequence 163 AA;
Query Match 75.1%; Score 750; DB 1; Length 163;
Best Local Similarity 70.3%; Pred. No. 9,22e-51;
Matches 97; Conservative 25; Mismatches 13; Indels 3; Gaps 1;
Db 1 MGWSCIIFFLVATATGHSQVQLQSGPELVKPGYVKRISKSGSYTFDAIHVKESH 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDVAIQWVQAP 60
Db 61 AKSLMEIGVTSAGDTNRYNOKFKKATMTVDKSSNTAYLELRLTSDSAIYVCARGW 120
QY 61 GGGLEWIGVINYIDNTNRYNOKFKKATMTVDKSTSTAYMELSSLRSEDTAVYICARAAW 120
Db 121 LLSFDYWGQGTTLTVSS 138
QY 121 YM---DYWGQGTTLTVSS 135
RESULT 11
ID R06369 standard; Protein: 135 AA.
AC R06369;
DT 13-DEC-1990 (first entry)
DE Anti-Tac heavy chain variable region.
KW anti-p55 Tac immunoglobulin (Ig) heavy chain; humanised Ig;
KW Interleukin-2 (IL-2); treatment of T-cell mediated disorders.
FH Key Location/Qualifiers
FT protein 20..135
FT /label=mature heavy chain
FN MO9007861-A.
PN 26-JUL-1990.
PD 28-DEC-1989; U05857.
PR 28-DEC-1988; US-290975.
PR 13-FEB-1989; US-310252.
PA (PROT-) PROTEIN DESIGN LABS.
PI Queen CL, Sellick HE;
DR WPI: 90-253800/33.
DR N-PSDB: Q05600.
PT Chimaeric immunoglobulin(s) blocking IL-2 binding to receptors -
PT comprising human framework and murine complementary determining
PT regions, less immunogenic than murine antibodies
PS Disclosure: P: English.
CC The sequence was prepared based upon a comparison of human antibody
CC EU and human anti-Tac Ab. It is the same as the EU sequence except
CC at certain defined regions. These are CDRs (amino acids 31-35,
CC 50-66 and 99-106), positions at which the EU residue (posn.s 27, 93,
CC 95, 98, 107-109, 111), posn.s immediately adjacent to a CDR of
CC anti-Tac (posn.s 30 and 67) and where the amino acid was thought to
CC have close proximity to the antigen-binding site (posn.s 48-68).
CC Humanised Ig's can bind to IL-2 receptors. They are not significantly
CC immunogenic in humans, are easily and economically produced and
CC have a longer half-life in vivo than murine antibodies. They are
CC useful, optionally attached to a cytotoxic agent, for treatment of
CC T-cell mediated disorders such as graft or transplant rejection.
CC See also Q05601.
SQ Sequence 135 AA;
Query Match 74.9%; Score 748; DB 1; Length 135;
Best Local Similarity 77.8%; Pred. No. 1.35e-50;
Matches 105; Conservative 14; Mismatches 16; Indels 0; Gaps 0;
Db 1 MGWSCIIFFLVATATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDVAIQWVQAP 60
QY 1 MGWNCIIFFLVTTATGHSQVQLVQSGAEVKKRPGSSVKVSKASGYTFDVAIQWVQAP 60

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OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:22:59 ; Search time 838.43 Seconds
(without alignments)
842.932 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396
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Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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1: gb_dal: *
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29: em_sy: *
30: em_un: *
31: gb_v1: *
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37: em_hum3: *
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48: em_hum5: *
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53: gb_htg10: *
54: gb_htg11: *
55: gb_htg12: *
56: gb_htg13: *
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64: em_htg6: *
65: em_htg7: *
66: em_hum6: *
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69: gb_htg20: *
70: gb_htg21: *
71: gb_htg22: *
72: gb_htg23: *
73: gb_htg24: *
74: gb_htg25: *
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81: gb_v11: *
82: gb_v12: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340	85.9	462	12	M28833 Mus musculus
2	340	85.9	480	5	A13733 Mus musculus
3	336.2	84.9	406	12	U62050 Mus musculus
4	333.6	84.2	419	12	U97570 Mus musculus
5	332	83.8	940	5	A44968 Mus musculus
6	332	83.8	940	5	I64459 Mus musculus
7	301.4	76.1	401	12	MMLA21LEY
8	298.2	75.3	402	12	MUSIGKALV
9	296	74.7	336	12	AF163745 Mus musculus
10	296	74.7	336	12	MDIGKVAR
11	296	74.7	339	12	AB028876 Mus musculus
12	295.2	74.5	408	12	S81289 Mus musculus
13	295	74.5	339	12	MUSIGKALV30
14	292.8	73.9	336	12	MDIGKVAL
15	292.8	73.9	336	12	MDIGKVAL
16	288.6	72.9	399	5	A47611 Sequence 3
17	288.6	72.9	399	5	A47611 Sequence 3
18	286.4	72.3	336	12	MMJ222607
19	286.4	72.3	337	12	S74056
20	285.4	72.1	439	5	A62621
21	285.4	72.1	439	5	A62621
22	284.8	71.9	366	12	MMIRACTV
23	284.8	71.9	336	12	MUSIGKADV
24	284.8	71.9	336	12	MUSIGKADV

25	284.8	71.9	339	12	MMU60464	U60464 Mus musculus
26	284.4	71.8	336	12	MMU55647	U55647 Mus musculus
27	284.2	71.8	336	12	MMU55674	U55674 Mus musculus
28	283.2	71.5	336	12	MDIGKXAO	Z22060 M. domestica
29	281.8	71.2	366	12	MMU15982	Y15982 Mus musculus
30	281.4	71.1	366	12	MMU55673	U55673 Mus musculus
31	280.6	70.9	399	12	MUSFABA	M95574 Mus musculus
32	279.8	70.7	411	12	MMIGGVJ5	X02181 M. musculus
33	279.8	70.7	1443	5	AR063210	AR063210 Sequence
34	279	70.5	427	5	AR04042	A94042 Sequence 23
35	279	70.5	8068	5	A94046	A94046 Sequence 27
36	278.4	70.3	336	12	MUSIGKADM	M37024 Mouse Ig re
37	278	70.2	336	12	MMU55675	U55675 Mus musculus
38	277.8	70.2	747	14	AC013153	AJ131533 Synthetic
39	277.6	70.1	336	12	MDIGKXAB	Z22023 M. domestica
40	277.2	70.0	881	12	MUSIGRCLA	L27438 Mouse Immun
41	275.8	69.6	870	5	AR063208	AR063208 Sequence
42	275.4	69.5	375	12	MMIGLCHVJ	X59816 M. musculus
43	274.2	69.2	926	12	RNIGKX3	X16129 Rat mRNA fo
44	274	69.2	330	12	MDIGKVBX	Z22131 M. domestica
45	273.6	69.1	667	12	MMU62649	U62649 Mus musculus

ALIGNMENTS

RESULT 1
MUSIGKPALI LOCUS MUSIGKPALI 462 bp mRNA ROD 18-NOV-1994
DEFINITION Mus musculus Igk chain (anti-Pseudomonas aeruginosa lipoprotein I antibody) mRNA, 5' end.
ACCESSION M28833.1 GI:576599
VERSION V-segment: anti-lipoprotein antibody; immunoglobulin kappa-chain; immunoglobulin light chain.
KEYWORDS Mus musculus (strain BALB/c, sub-species domesticus) hybridoma CDNA to mRNA.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 462)
AUTHORS Margel, M., Eckhardt, A., Ehret, W., von Specht, B. U., Duchene, M. and Domdey, H.
TITLE Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas aeruginosa outer membrane protein I
JOURNAL Gene 74 (2), 335-345 (1988)
COMMENT 89232725
MEDLINE On Nov 28, 1994 this sequence version replaced gi:342017.
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Location/Qualifiers
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/cell_line="Mab 6A4"
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/product="immunoglobulin kappa chain"

gene
mat_peptide

BASE COUNT	114 a	116 c	121 g	111 t
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Query Match	85.9%; Score 340; DB 12; Length 462;			
Best Local Similarity	91.2%; Pred. No. 3.9e-107;			
Matches 361; Conservative	0; Mismatches 35; Indels 0; Gaps 0;			
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DB	19 atgagttcacagcccccaggtcttctatgtcgtcgtcgtatggtatcgtcgtggtg 78			
QY	61 gacatgtctgacacagtcctcagaatccctggtcgtgtaagttaggaagagggccact 120			
DB	79 gacattgtatgtcacagtcctcagaatccctggtcgtgtaagttaggaagagggccact 138			
QY	121 attagctgaatcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180			
DB	139 atgagctgcgaatccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 198			
QY	181 tggctacacagagaaacacagagcagctccttaactgctgctatctatggtcagtcag 240			
DB	199 tggctacacagagaaacacagagcagctccttaactgctgctatctatggtcagtcag 258			
QY	241 gaatctggagtcctcgtatcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 300			
DB	259 gaatctggagtcctcgtatcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 318			
QY	301 atcagcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 360			
DB	319 atcagcagtcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 378			
QY	361 tacagcttcgagacaggggacagagtcgagacagagtcgagacagagtcgagacag 396			
DB	379 cggacgttcgagacaggggacagagtcgagacagagtcgagacagagtcgagacag 414			
RESULT 2				
LOCUS A13733 480 bp DNA PAT 03-JAN-1994				
DEFINITION variable region of a monoclonal antibody which cross reacts with 19 known P.aeruginosa serotypes.				
ACCESSION A13733				
VERSION A13733.1 GI:491741				
KEYWORDS synthetic construct.				
ORGANISM synthetic construct.				
REFERENCE 1 (bases 1 to 480)				
AUTHORS Domdey, H., Margel, M. and von Specht, B. U.				
TITLE Monoclonal antibodies to Pseudomonas aeruginosa, their production and use				
JOURNAL Patent: EP 038395-A 1 25-OCT-1989;				
BEHRINGERWERKE Aktiengesellschaft				
FEATURES Location/Qualifiers source 1..480 /organism="synthetic construct" /db_xref="taxon:32630" 37..>480 /codon_start=1 /transl_table=11 /product="V region of a monoclonal antibody, cross reacts with 19 P. aeruginosa serotypes" /protein_id="CAA01126.1" /db_xref="GI:491742" /translation="MDSQAVLILLWVSGTCDIVMSQSPSSLAWSAGEKVTMSCKSSQSLNSTRKFLAWYQKQSGSPKLLIYASRSGVPRFTSGSGSDFTLTISSVQADLAVYCKOSYNLRTFGGKRLIKRADAPVTSIFPPCE"				
BASE COUNT 115 a 117 c 136 g 112 t				
ORIGIN				
Query Match	85.9%; Score 340; DB 5; Length 480;			

Best Local Similarity 91.2%; Pred. No. 3.9e-107;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 atgagatcaagagccaggtctctatattctgtctgtataggtatctgtcactgtggg 60
DB 37 ATGATTCACAGGCCGCGTCTTATATGCTGCTGATGGATCTGTGACTGTGGG 96
QY 61 gacatgtgtgacacagctccagattccctgtctgtaagcttagagagagggcact 120
DB 97 GACATTTGATGACAGTCTCCATCTCCCTGCTGTGTCAGACAGGAGAGAGGTACT 156
QY 121 atgagtcgaatccagctcagctcagctcagctcagctcagctcagctcagctc 180
DB 157 ATGAGTCGAATCAGTCAAGTCTGCTCAACAGTATTAACCCGAAGAATCTTGGCT 216
QY 181 tggtaacagagaacacagagagagagagagagagagagagagagagagagag 240
DB 217 TGGTACACAGAGAAACAGGAGCACTCTAACTGCTGATCTACTGGGCACTAGG 276
QY 241 gaatctgggtccctgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
DB 277 GAATCTGGGTCCCTGATCTGCTTACAGGCACTGATCTGGGACAGATTTACTCTCAC 336
QY 301 atcagcagctcagcagctcagcagctcagcagctcagcagctcagcagctc 360
DB 337 ATCAGCAGTGTGACAGGCTGAAGACCTGGAGTTTATTAAGTCAAGCAATCTTAACTT 396
QY 361 tacagctcagcag 396
DB 397 CGGACGTTGCGTGGAGGACCAAGCTGGAATCAAA 432

RESULT 3

LOCUS MMU62050 406 bp mRNA ROD 19-FEB-1997
DEFINITION Mus musculus polyreactive autoantibody, immunoglobulin light chain
ACCESSION U62050
VERSION U62050.1 GI:1438580

SOURCE

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
Dighiero,G.
Structural and affinity studies of IgM polyreactive natural
autoantibodies

J. Immunol. 158 (2), 968-976 (1997)
97146071

REFERENCE
AUTHORS Diaw,L., Magnac,C., Pritsch,O., Buckle,M., Alzari,P.M. and
Dighiero,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et
d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
75724 Paris Cedex 15, France

FEATURES

source

1. 406
/organism="Mus musculus"
/strain="(CBA/NXBALB/c)F1"
/db_xref="taxon:10090"
/sex="male"
/note="hybridoma M25-9; 6-day-old spleen cells fused with
SP2/0 myeloma cells"
<1. >406
/codon_start=1
/product="polyreactive autoantibody, immunoglobulin light
chain kappa"
/protein_id="AAB47613.1"
/db_xref="GI:1438581"
/translation="QVILLILLWVSGTCDIYVSGSPSLAVSAGEKVTMSCKSSQSL

CDS

BASE COUNT 101 a 99 c 108 g 98 t
ORIGIN
LNSRTRNYLAMYQAKPGQSPKLLIYMASTRRESGVDPFRFTSGSGTDFLTLTSSVQAE
DLAVYCKOSYNLYTFGGGTKEIKRADAPV"

Query Match 84.9%; Score 336.2; DB 12; Length 406;
Best Local Similarity 92.7%; Pred. No. 8e-106;
Matches 353; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 16 caggtctctatattgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 75
DB 1 CAGGTCTTATATGCGTGTGATGGTATCTGTACTGCGGACATGATGATGCA 60
QY 76 cagctccagattccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 135
DB 61 CAGTCTCAATCCTCCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 136 agtcagagctgtctcaacagtagaacccagagagagagagagagagagagagag 195
DB 121 AGTCAGAGTCTGCTCAACAGTAGAACCCGAAGAACTTGTGGCTGTACACAGAAA 180
QY 196 ccaagggagccctcctaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 255
DB 181 CCAGGCGAGTCTCTTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 256 gatcgctcagtgagcagtgatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 315
DB 241 GATGCTTCAAGGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 316 gctgaagacgtgtgagatttactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 375
DB 301 GCTGAAGACCTGCGAGATTATTAAGTCAAGCAATCTTATATCTGTACACCTTGGAGGG 360
QY 376 gggacccaaggtggaataaaa 396
DB 361 GGGACCAAGCTGGAGATAAAA 381

RESULT 4

LOCUS MMU97570 419 bp mRNA ROD 11-JUN-1997
DEFINITION Mus musculus immunoglobulin light chain variable region (IgK) mRNA,
partial cds.
ACCESSION U97570
VERSION U97570.1 GI:2183076

KEYWORDS

SOURCE

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 419)
Feljo,G.C.S., Sabadga,J., Carneiro,C.R.W. and Brigido,M.M.
Variable region structure and staphylococcal protein A binding
specificity of a mouse anti-laminin receptor monoclonal IgM

Immunology (1997) in press
2 (bases 1 to 419)
Brigido,M.M.
Direct Submission
JOURNAL Submitted (15-APR-1997) Biologia Celular, Universidade de Brasilia,
Campus Universitario, Asa Norte, Brasilia, DF 70910-900, Brazil

FEATURES

source

1. 419
/organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
/cell_line="1H12"
/cell_type="hybridoma"
1. >419
/gene="IgK"
21. >419
/gene="IgK"
/note="rearranged Vh8 to Jk1 region"

CDS

gene
1. >419
/gene="IgK"
21. >419
/gene="IgK"
/note="rearranged Vh8 to Jk1 region"

/codon_start=1
/product="Immunoglobulin light chain variable region"
/protein_id="AAB60862.1"
/db_xref="GI:2183077"
/translation="MDSQAOYLILLIILVSGTCDITVMSQSPSLVAGEKWTMSCK
SSQSLKSRTRNYLAWYQKRGQSPKLLIYWASRESGVDPDRFGSGSDFTLTIS
SVQADDLAIYCKQSYNLRTFGGPKLEIKR"
BASE COUNT 105 a 101 c 115 g 98 t
ORIGIN

Query Match 84.2%; Score 333.6; DB 12; Length 419;
Best Local Similarity 90.2%; Pred. No. 6.5e-105;
Matches 357; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 atgagttcaagagccaggttcttatatgtcgtcgtatgtatgtatcgtgacccgtggtg 60
|||||
DB 21 ATGGATTTCACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGTCGTGGG 80
QY 61 gacattgtctgacacagctccagatccctggtcgttaagcttaagagagagggccact 120
|||||
DB 81 GACATTGTATGTACAGTCTCATCTCTCCCTGCTGTGTGTCAGCAGGAGAGAGAGTCACT 140
QY 121 attagctgcaaatccagtcagagctcgtcctcaacagtagaaccgagagaaactatgtgt 180
|||||
DB 141 ATGAGCTGCAAGTCCAGTCCAGATGCTCAAAAGTAGAACCCGAGAGATTACTTGCT 200
QY 181 tggtaaccagagaaccagagggcagcctcctaaactgtatctactcgtggcatccactag 240
|||||
DB 201 TGGTACCAAGCAAAACCAAGGAGTCTCCCAACCTGCTATCTACGCGCATCCACTAGG 260
QY 241 gaatctgggtccctgagctcagctcagtgagtgagtcgtggagacagattcactccacc 300
|||||
DB 261 GAATCTGGGGTCCCTGATGCTTTCACAGCAGTGGATCTGGGACAGATTTCACCTCCACC 320
QY 301 atcagcagctctgcaagctgaaagcgtgagcttatactactgacgcaatctataatctt 360
|||||
DB 321 ATCAGCAGTGTGTCAGGCTGAGACCTGGCAATTATTACTGCAAGCAATCTATATCTT 380
QY 361 tacagcttcgagcagggagcgaaggtgggaataaaa 396
|||||
DB 381 CGGACGTTGCTGGTAGAGGCCCAAGCTGGAATCAAA 416

RESULT 5
LOCUS A44968 940 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 24 from Patent W09515382.
ACCESSION A44968
VERSION A44968.1 GI:2299554
KEYWORDS
SOURCE
ORGANISM
unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
ZENECA LTD (GB)
Other publication GB 2297751 960814
Other publication CA 2174972 950608
Other publication ZA 9409266 950605
Other publication AU 1113095 950619.
FEATURES
source
1..940
/organism="unclassified"
/db_xref="taxon:32644"
BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match 83.8%; Score 332; DB 5; Length 940;
Best Local Similarity 89.9%; Pred. No. 2.6e-104;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Best Local Similarity 89.9%; Pred. No. 2.6e-104;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 atgagttcaagagccaggttcttatatgtcgtcgtatgtatgtatcgtgacccgtggtg 60
|||||
DB 10 ATGGATTTCACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGTCGTGGG 69
QY 61 gacattgtctgacacagctccagatccctggtcgttaagcttaagagagagggccact 120
|||||
DB 70 GACATTGTATGTACAGTCTCATCTCTCCCTGCTGTGTGTCAGCAGGAGAGAGTCAAC 129
QY 121 attagctgcaaatccagtcagagctcgtcctcaacagtagaaccgagagaaactatgtgt 180
|||||
DB 130 ATGAGCTGCAAGTCCAGTCCAGTCTCCCTCAACAGTAGAACCCGAGAGATTACTTGCT 189
QY 181 tggtaaccagagaaccagagggcagcctcctaaactgtatctactcgtggcatccactag 240
|||||
DB 190 TGGTACCAAGCAAAACCAAGGAGTCTCCCAACCTGCTATCTACGCGCATCCACTAGG 249
QY 241 gaatctgggtccctgagctcagctcagtgagtgagtcgtggagacagattcactccacc 300
|||||
DB 250 ACATCTGGGGTCCCTGATGCTTTCACAGCAGTGGATCTGGGACAGATTTCACCTCCACC 309
QY 301 atcagcagctctgcaagctgaaagcgtgagcttatactactgacgcaatctataatctt 360
|||||
DB 310 ATCAGCAGTGTGTCAGGCTGAGACCTGGCAATTATTACTGCAAGCAATCTATATCTT 369
QY 361 tacagcttcgagcagggagcgaaggtgggaataaaa 396
|||||
DB 370 CGGACGTTGCTGGTAGAGGCCCAAGCTGGAATCAAA 405

RESULT 6
LOCUS I64459 940 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5665357.
ACCESSION I64459
VERSION I64459.1 GI:2481353
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Antibodies recognizing tumor associated antigen CA 55.1
Patent: US 5665357-A 24 09-SEP-1997;
FEATURES
source
1..940
/organism="unknown"
BASE COUNT 241 a 266 c 213 g 220 t
ORIGIN

Query Match 83.8%; Score 332; DB 5; Length 940;
Best Local Similarity 89.9%; Pred. No. 2.6e-104;
Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 atgagttcaagagccaggttcttatatgtcgtcgtatgtatgtatcgtgacccgtggtg 60
|||||
DB 10 ATGGATTTCACAGGCCAGGTTCTTATATGCTGCTGCTATGGGTATGTCGTGGG 69
QY 61 gacattgtctgacacagctccagatccctggtcgttaagcttaagagagagggccact 120
|||||
DB 70 GACATTGTATGTACAGTCTCATCTCTCCCTGCTGTGTGTCAGCAGGAGAGAGTCAAC 129
QY 121 attagctgcaaatccagtcagagctcgtcctcaacagtagaaccgagagaaactatgtgt 180
|||||
DB 130 ATGAGCTGCAAGTCCAGTCCAGTCTCCCTCAACAGTAGAACCCGAGAGATTACTTGCT 189
QY 181 tggtaaccagagaaccagagggcagcctcctaaactgtatctactcgtggcatccactag 240
|||||
DB 190 TGGTACCAAGCAAAACCAAGGAGTCTCCCAACCTGCTATCTACGCGCATCCACTAGG 249

241 gaatctgggtccctgatacgtcagctggcagctgagatcctggacagattcactcacc 300
|||||
Db 250 ACATCTGGGGTCCCTGATCGCTTCACAGGCGAGTGGATCTGGGACAGATTCTCTCACC 309
|||||
QY 301 atcagcagctcgcagctgtaagacgctgacagcttattactcagcagcaattcattacc 360
|||||
Db 310 ATCAGCAGTGTGAGAGGCTGGAAGACCTGGCAATTTATTACTGCAGACATCTTATCTCTT 369
|||||
QY 361 tacacgtctggacaggggaccaggttggaataaa 396
|||||
Db 370 CGGACGTTGGGTGGAGCCACCAGCTGGAAATCAAA 405
|||||

RESULT 7
MMLA2JILEV 401 bp DNA ROD 15-JUN-1993
LOCUS M.musculus DNA for Ige antibody light chain (VJ).
DEFINITION X65774
ACCESSION X65774.1 GI:312076
VERSION Ige antibody; J-segment; light chain; V-region.
KEYWORDS mouse mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Kofler, H., Schnegg, I., Geley, S., Helmling, A., Varga, J.M. and
Kofler, R.
TITLE Mechanism of allergic cross-reactions--III. cDNA cloning and
variable-region sequence analysis of two Ige antibodies specific
for trinitrophenyl
Mol. Immunol. 29 (2), 161-166 (1992)
JOURNAL 92178225
MEDLINE
FEATURES
source Location/Qualifiers
1. 401
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="IGEL2 (ATCC-TIB142)"
3. .>401
/codon_start=1
/product="Ige antibody light chain (VJ)"
/protein_id="CAA658.1"
/db_xref="GI:312077"
/translation="MDSQAOYMLLLMWSGTCGDYMSQSPSSLAIVSGEYKTMSC
SSOSLIYSSNQKNTLAWYQKPGQSPKLLIYMASTRSGVPDRFSGSGSTDTLTIS
SVRAEDLAVYICQYINPSTFGGYLEIK"
3. .>401
V-region
/product="Ige antibody light chain (VJ)"
sig_peptide 3. 62
J-segment 365. .>401
BASE COUNT 100 a 91 c 105 g 105 t
ORIGIN

Query Match 76.1%; Score 301.4; DB 12; Length 401;
Best Local Similarity 86.5%; Pred. NO. 1e-93;
Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 1 atgattcacagcagcagctctatattgctgctgctatgctgacacctgtgg 60
|||||
Db 3 ATGACTTCACAGGCCGAGCTCTATGTACTGCGCATGGTATCTGTACCTGTGG 62
|||||
QY 61 gacattgtcgtacacagctccagatccctgctgtaagccttagagagagggccac 120
|||||
Db 63 GACATTGTGATGTCACAGTCTCCATCCCTAGCTGTGAGTGGAGAGAGGTACT 122
|||||
QY 121 attagctgcaaaatcagctcagatcgtctcaacagtagaaccgagaaactactgt 180
|||||
Db 123 ATGAGCTGCAGTCAGTCAGGCTTTTATATAGTACCAATCAAAAGACTTGGCC 182
|||||
QY 181 tgcattacagcagaacacagcagcctcctcctaactgctgactactggtgacactag 240
|||||
Db 183 TGTATACAGCGGAACACAGGCGAGTCTCTTAAGTGTGATTTACTGGCATCCACTAG 242
|||||

241 gaatctgggtccctgatacgtcagctggcagctgagatcctggacagattcactcacc 300
|||||
Db 243 GAATCTGGGGTCCCTGATCGCTTCACAGGCGAGTGGATCTGGGACAGATTCTCTCACC 302
|||||
QY 301 atcagcagctcgcagctgtaagacgctgacagcttattactcagcagcaattcattacc 357
|||||
Db 303 ATCAGCAGTGTGAGAGGCTGGAAGACCTGGCAATTTATTACTGCAGACATCTTATAGCTCT 362
|||||
QY 358 cttaacagcttggacaggggaccaggttggaataaa 396
|||||
Db 363 CCGTACAGTTCGAGGAGGCGGACCAGCTGGAAATATAA 401
|||||

RESULT 8
MUSIGKALA 402 bp mRNA ROD 14-JUL-1993
LOCUS Mouse Ig rearranged K-chain mRNA V-region, 5' end.
DEFINITION M98042
ACCESSION M98042.1 GI:196749
VERSION V-region; hepatitis; immunoglobulin light chain; processed gene.
KEYWORDS Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to
mRNA.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Hong, H.J., Kim, A.K., Ryu, C.J., Park, S.S., Chung, H.K., Kwon, K.S.,
Kim, K.L., Kim, J. and Han, M.
TITLE Cloning and characterization of cDNA's coding for heavy and light
chains of a monoclonal antibody specific for pre-S2 antigen of
hepatitis B virus
hepatitis B virus
Gene 121, 331-335 (1992)
JOURNAL 93077049
MEDLINE
FEATURES
source Location/Qualifiers
1. 402
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="H8"
/cell_type="hybridoma"
/tissue_type="spleen"
/map="Chromosome 6"
1. 60
sig_peptide 1. 402
CDS
1. 402
/partial
/codon_start=1
/function="specific for pre-S2 antigen of hepatitis B
virus"
/product="immunoglobulin kappa-chain"
/protein_id="AAA38777.1"
/db_xref="GI:196750"
/translation="MDSQAOYMLLLMWSGTCGDYMSQSPSSLAIVSGEYKTMSC
SSOSLIYSSNQKNTLAWYQKPGQSPKLLIYMASTRSGVPDRFSGSGSTDTLTIS
SVRAEDLAVYICQYINPSTFGGYLEIK"
61. 402
mat_peptide /partial
BASE COUNT 102 a 93 c 100 g 107 t
ORIGIN

Query Match 75.3%; Score 298.2; DB 12; Length 402;
Best Local Similarity 86.0%; Pred. NO. 1.3e-92;
Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 atgattcacagcagcagctctatattgctgctgctatgctgacacctgtgg 60
|||||
Db 1 ATGATTTCACAGGCCGAGCTCTATGTACTGCTGATGGTATCTGTACCTGTGG 60
|||||
QY 61 gacattgtcgtacacagctccagatccctgctgtaagccttagagagagggccac 120
|||||
Db 61 GACATTGTGATGTCACAGTCTCCATCCCTAGCTGTGTCAGTTGGAGAGAGGTACT 120
|||||

Cy	121	atgagtcgaatccagtcagagctctgtcaacagtagaacccgagagaaactactcttggct	180
Db	121	ATGAGCTCAGTCCAGTCAGCAGAGCCTTTTATATGTAGCAATTAAAAAGACTCTTGGCC	180
Cy	181	tgtataccagcagaacccaagggcagcctctctaaactgtcatctacttggcaccactag	240
Db	181	TGTTACCCAGCGAAGAAACCGGGCACTTCTCTAAATGCTGTATTACGGGCATCCACTAGG	240
Cy	241	gaatctggggcccttgatcgcctctagcttagtggcagctgagctcgtgagcaaatcactccacc	300
Db	241	GAATCTGGGGCTCCTGATCGCTTACACGCGAGCTGGATCTTAGACAGATTTTCATCTCACC	300
Cy	301	atcagcagctctgcagcgctgaaagacgtgycagttatatactgcagcaaatctata---at	357
Db	301	ATCAGCAATGTGAAGGCGCTGAGACCTGGCAGTTATTACTGTACGCAATATTATTAACTAT	360
Cy	358	cttcaacagttcgcagacaggggacccaagggtagaataaataaa	396
Db	361	CCGTCACAGCTTCGAGAGGGGGACCTTACTGTGAATAATAAA	399

RESULT	9
AF163745	
LOCUS	AF163745 336 bp mRNA
DEFINITION	Mus musculus mab 27.4.1 immunoglobulin light chain variable region
VERSION	AF163745 partial cds.
ACCESSION	AF163745.1 GI:5690296
KEYWORDS	
SOURCE	house mouse.

REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS TITLE
1 (bases 1 to 336) Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W. Molecular Analysis of Crossreactive Anti-Myosin/Anti-Streptococcal Mouse Monoclonal Antibodies	Unpublished
2 (bases 1 to 336) Mertens, N.M. and Cunningham, M.W. Direct Submission	2 (bases 1 to 336) Mertens, N.M. and Cunningham, M.W. Direct Submission
	Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma

FEATURES	Location/Qualifiers
source	1. .336

CDS

BASE COUNT	91 a	83 c	86 g	76 t
ORIGIN				

Query Match	74.78;	Score 296;	DB 12;	Length 356;
Best Local Similarity	92.68;	Pred. No. 7.5e-92;		
Matches 311; Conservative	0;	Mismatches 25;	Indels 0;	Gaps 0;

Oy 61 gacattgtcgtcacacagctctccagatccctcgctgtaagctaaggagaagggcaact 120
||||||| ||||||| ||||||| ||||||| |||||||
Db 1 GACATTGTGATGTCAACAGTCTCCCATCCTCCCCTGGCTGTCTCAGCAGGAGAAGAGTCACT 60

QY 121 attagctgcaaatccagtcagagtcgtctcaacagtagaacccgagagaactacttgct 180

Db	61	ATGAGCTCAATATCCAGTCAAGTCTGCTCAACAGTGAACCCGAAAGACTACTTGCT	120
Oy	181	tgtatccagcagaaacacagggcagccctcctaaactgtgtatctacttggatcatcagg	240
Db	121	TGTATCCAGCAAAACCAAGGCACTTCTTAACTGTAATCTGATCTACTGGCATCCACTAGG	180
Oy	241	gaatctggggtcccttgatcgcttcagtgtgcagtygatctcggacagatctcaactcac	300
Db	181	GAATCTGGGGTCCCTTGATCGCTTCAACAGGCAAGTGAATCTGGAGATTCCTCAACC	240
Oy	301	atccagcagctcccgaggtctgaagaagttgacglttatctatctgcacgcaatcttaactc	360
Db	241	ATCAGCACTGTGCAGGCGTGAAGACTCTGGCATTTATTAATCAAGCAATCTTAAATCTG	300
Oy	361	tacacgttcgcagcagggagaccagaagtggaaataaa	396
Db	301	TACAGTTCCGAGGGGGGACCAACTGGAATAA	336

RESULT	10			
MDIGKVAR				
LOCUS		336 bp	mRNA	
DEFINITION	M.domesticus	Igk variable region.		
ACCESSION	222063			
VERSION	222063.1	GI:297629		
KEYWORDS	anti-DNA antibody; Igk gene; Igk variable region; Immunoglobulin.			
SOURCE	western European house mouse.			
DATE				05-NOV-1994

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE
1 (bases 1 to 336)	Tillman, D. M.,	Hill, R. J. and Marion, T. N.	Both IgM and IgG anti-DNA antibodies are products of clonally selective B cell stimulation in (NZB x NZW)F1 mice	J. Exp. Med.	176 (3), 761-775 (1992)
9238144					
2 (bases 1 to 336)					

AUTHORS	TITLE
Marion, T. N.	Direct Submission
Submitted (23-MAR-1993)	Tony N. Marion, Microbiology and

FEATURES	Location/Qualifiers
source	1. 336

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<1..>336
CDS

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antibody: VK8 family"
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Query Match	74.78; Score 296; DB 12; Length 336;
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Query Match	74.58%	Score 295.2	DB 12	Length 408
Best Local Similarity	84.18%	Pred. No. 1.5e-91		
Matches 333	Conservative	0	Mismatches 63	Indels 0
				Gaps 0

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Db	7	ATGGAAATACAGACACAGAGTCTCTCATGTGCCGTGCTCTGGGTATCTGGTACCTGTGGG	66
QY	61	gacattctgctcacacagctctccagattccctgcgtgtlaagctllaggaagagggccact	120
Db	67	GACATTGTGATATACCCAGACTCCATTCCTCCGCCGTGTCCAGCAGGGGAGAAAGGTCACT	126
QY	121	attagctgcacaatccagctcagatcagatctctgcacagtaagaccgagagaactattgct	180
Db	127	ATGACCTCCAGATCCAGATCAGAGTCTTTTATTCATATGAAACAAAAAGAACTACTTGGCC	186
QY	181	tgtttcccgagcaaaacccaggcgagcgtctcttaacgtgcctgatatgtgacatccactgg	240
Db	187	TGTATCCAGCAAAACCCAGGGCAGTCTCTTAATCTGCTATTTACTGGGCATCCACTAGG	246
QY	241	gaatctgggtgccctgcgatcgcgtctcaagtgcagtgagtcctggaacagattcaactccacc	300
Db	247	GAATCTGGGGTCCCTGATTCGCTTCATTAGGCAATGGATCTGGGACAGATTTCCTGTGACC	306
QY	301	atcagcagctctgcagagcttgaagacgctggcagttatctactgcacgaacatctataactt	360
Db	307	ATCACCAATGTGTCAAGCAGAAACCTGGCTGTTTATTTACTGCCACACAGACTATTAACCTTG	366
QY	361	tacagcttcgagcaagggaacccaagttgnaataaaaaa	396
Db	367	TTCACGTTTGGAGCTGGGACCAGAGCTGGGAACATGAAA	402

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RESULT 13
MUSIGKV130
LOCUS      339 bp      mRNA      ROD      29-OCT-1994
DEFINITION Mus musculus Ig rearrange kappa-chain gene V19-J1 region.
ACCESSION  L16819
VERSION     L16819.1  GI:293622
KEYWORDS    V-region; complementarity determining region; immunoglobulin light
            chain; kappa-immunoglobulin; processed gene.
SOURCE      Mus musculus (strain NZB/W F1) mRNA.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 339)
AUTHORS     Justgarten,D.L., Kavalier,J., Gerhard,W. and Scharff,M.D.
TITLE       The response to a foreign antigen in the autoimmune NZB/W F1 murine
            strain
JOURNAL     Unpublished (1993)
FEATURES    Location/Qualifiers
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            148..168

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	/standard_name="J1"	
BASE COUNT	89 a 85 c	76 t
ORIGIN		1 others

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Best Local Match	Similarity	92.3%	Pred. No. 1.7e-91:		
Matches 310:	Conservative	0:	Mismatches 26:	Indels	Gaps
QY 61	gacattgctgcgacacacatccacagatcccttgctctgtaagcttagagaaagggccact				
Db 1	GACATTGTGATGTGCACACTCTCCATCTCCCTCGCTGTCTGACGAGSAGAGGGTCACT				
QY 121	attagctgcaaatccacgtccagatcagatctgtctcaacagtagaacccgagagaacttggct				
Db 61	ATGAGCTGCAATCCAGTCAGACAGTCTGCTCAACAGTAGAACCCGAGGAACTACTTGACT				
QY 181	tgtgtaccggcagaaacccggcgacgctctctaactgtcgatctctactgtggcactcaatgg				
Db 121	TGTGTACCGACGAAACCAGGGSCATGCTCTTAACGTGCTGATCTACTGGGCACTCACTAGG				
QY 241	gaatctgggtgcacctgacatcgctctcaatgctgacgtgatcttggaacagattcaactcacc				
Db 181	GAACTGGGGGTCCCGATCGCTTCAACAGCAGTGGATGTGGGACAGATTTCATCTCAAC				
QY 301	atcagcagctctgcagagctgaaagacgltgycagtttattactctgcaacgcaactctataatct				
Db 241	ATCAGCACTGTGCAGGGCTGAAGACCTGGCACTTTATTTACTGCAAGCAATCTTATATCT				
QY 361	tacacgttcggacagcgggacccaagttggaataaa		396		
Db 301	TACACGTTTCGGAGGGGAGCAACGCTGGAATAATAAA		336		

RESULT 14	MDIGVAL	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES		
		MDIGVAL	M.domesticus Igg variable region.	222039	222039.1	GI:297576	anti-DNA antibody; Igg gene; Igg variable region; Immunoglobulin.	Mus musculus domesticus	Western European house mouse.	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Scurionata; Muridae; Murinae; Mus.	1 (bases 1 to 336)	Tilman,D.M., Jou,N.T., Hill,R.J. and Marlon,T.N.	Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice	J. Exp. Med. 176 (3), 761-779 (1992)	2 (bases 1 to 336)	Marlon,T.N.	Direct Submission	Submitted (23-MAR-1993) Tony N. Marlon, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA	Location/Qualifiers	1. 1336
																		/organism="Mus musculus domesticus" /strain="(NZB x NZW)F1" /isolate="mouse #163" /db_xref="taxon:10092" /chromosome="6" /sex="Female" /dev_stage="somatic variant"		

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gene      /tissue_type="spleen"
          /cell_type="hybridoma"
          /cell_line="163.1"
          1. .336
          /gene="Irf3"
          <1. .>336
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ORIGIN	82 c	88 g	76 t
90 a	<p> /product="immunoglobulin variable region" /protein_id="CA480013.1" /db_xref="gi:297577" /translation="DIVMSQSPSLAYSAGEKVTMSCKSSQSLNSRTKRNLYAWYQO KPGSGPKLLITWASSRSGVDRFTGSGDFLLTISVQAEIDLAVYIKQSYNLYT FGGGKLEIK" </p>		

Query Match	73.9%	Score 292.8;	DB 12;	Length 336;
Best Local Similarity	92.0%;	Pred. No. 9.8e-91;		
Matches 309;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;

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Oy  61  gacattgtgcgcacacagctctccagatctccctgctgtaagcttagagagagggcact 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   1  GACATTGTGATGTCACAGTCTCCATCCCTCCCTGGCTGTGTCCAGCAGGAGAGAAAGTCACT 60

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Dy 121 attgctgcgaatccagtcaggtctgtctaaccagtagaacccggagaaactacttgct 180
|||
Db 61 ATGAGCTGCAATCCAGTCAAGTGTCGTCAACAGTAGAACCCGAAGAAGACTACTTGGCT 120

Qy 181 tggtraccagcagaacaacgaggcgacctctaactgtctatctactgygcattccacagg 240
Db 121 TGGTACCAAGCAGAAACCAGGCGAGTCCTTAACACTGTATCTACTGGGCATCCAGTAGG 180

241 gaattcggggccccgacacgcttcagtcgagtcgattccggagacgatttcacttcacc 300
|||||
181 gaattcggggccccgacacgcttcacacagcagtcgattcgggacagatttcacttcacc 240

241 ATCAGCAGTGTGCAGGCTGAAGACCTGTGCACTTATTACTGCAGCAATCTTATAA^{CTG} 300

Db 301 TACACGTTCCGGGGGGACCAAGCTGGAATATAAA 336

MDIGKVAU	336 bp	mRNA	ROD	05-NOV-1994
MDIGKVAU				
LOCUS				
DEFINITION	M.domesticus Iak variable region			
RESULT	15			

RECESSION	
VERSION	ZZ2070
KEYWORDS	ZZ2070.1 GI:297635
SOURCE	anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin heavy chain constant region; western European house mouse.

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 336)

TITLE	Both IgM and IgG anti-DNA antibodies are the products of clonal selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL	J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE	92381444

REFERENCE 2 (bases 1 to 330)
AUTHORS Marlon, T. N.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1993) Tony N. Marlon, Microbiology and

Immunology, University of, Tennessee, Memphis, 858 Madison Avenue
Memphis, TN, 38163, USA

location/Qualifiers

1. .336

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CDS       <1. .>336

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antibody: Vk8_family"
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BASE COUNT	91 a	83 c	86 g	76 t
ORIGIN				

Query Match	73.9%;	Score 292.8;	DB 12;	Length 336;
Best Local Similarity	92.0%;	Pred. No. 9.8e-91;		
Matches 309;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0

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QY      61 gacatttgtctgacacagtcctccagaatcccctgtcgttaagttagyagagaggggccaact 120
          |||||
Db       1 GACATTGTGATGTACACAGTCTCCATCCTCCCTGGCTGTGCAGCAGAGAGAAAGTCACT 60
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QY 121 atcgcgtgcaatcccgatcagctctgttcaacagttagaacccggagaaacttctgct 180
Db 61 ATGAGCTGCATCCATGCAGAGTCTGCTCAACAGTAGAACC CGAAAGACTTA CTGGCT 120

101 cggctccacgacgaataccagggcagcccccacaatcgcgcgacccacgggacatccacagg 248
121 TGATCACGACGAATCCAGGCGAGTCTCTAACTGCTGATCTACTGGGCATCCACATAGG 180

Db 181 GAATCTGGGGTCCCTATCGCTTACACAGCAGTGTGGACAGATTTCCTCACC 240

Ov	361	tacagccttcctgacacaccccttgcgaataaaa	306
Db	241	ATCAGCAGTGTGCAGCGCTGAAACCTGGCAGTTATTACTGCAAGCAATCTATAA	CTG 300

Db 301 TACACGTCGAGGGGGGACCAAGCTGGAATATAA 336

Search completed: August 27, 2000, 06:23:02
Job time: 2484 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:08:49 ; Search time 864.98 seconds
(without alignments)
2018.881 Million cell updates/sec

Title: US-09-249-011-7
Perfect score: 396
Sequence: 1 atgattcacagcagccaggtf.....ggaccacagtggaataaaaa 396

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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QY	250	gtccctgtacgtcttcaatgtgacgtgatcttggtgagacgaattcaactccacatcagcagt	309
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QY	310	ctgcagcgtcgaagacgttgcagtttattactgcacgcacatcttaactct--tacag	366
DB	310	ctgcagagcgtgaaagatgtgcacgtttattactgtgcacgaatattcattgatttccgttacct	369
QY	367	ctcgcacagggagcacaagtgtggaataaa	396
DB	370	tttgccacagggagcacaagcttgagatcctaa	399
RESULT	4		
AM404610			
LOCUS	AM404610	550 bp	16-FEB-2000
DEFINITION	UI-HF-BL0-acc-a-06-0-UI.r1 NIH_MGC_37 Homo sapiens cdna clone		
ACCESSION	IMAGE:3058451 5', mRNA sequence.		
VERSION	AM404610		
KEYWORDS	AM404610.1 GI:6923667		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 550)		
COMMENT	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 486-1550 Email: Robert_Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLN at: www.bio.lnl.gov/dbip/image/image.html Seq primer: M13 Forward.		
FEATURES			
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BASE COUNT	140 a 150 c 139 g 121 t		
ORIGIN			
Query Match	57.2%	Score 226.6; DB 72; Length 550;	
Best Local Similarity	79.6%	Pred. No. 2.4e-59;	
Matches	281; Conservative	0; Mismatches 69; Indels 3; Gaps 1;	
DB	8	ctggagcctgtgtggaacattgtcgcgcacacatccacagatccctggtgtaagcttag	67

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Db	68	GGGAGAGGGGCCACCACTCACACTCAGATCGACGACAGAGTGTTTATACAGCTTCACAATA	127
Qy	167	agaactacttgctgtgtaccagcagaaacacagggcagccctcttaaatctgtact	226
Db	128	AGAATTACTTAGCTTGTAACAGCAGAAACCAGACAGACCTCCCTAACTGCATTTACG	187
Qy	227	gggatccaactaggggaacctggtgccctgtatgcattcaatgtgcagctgtggaaag	286
Db	188	GGGCACTCAACCCGGGAATCCGGGGTCCCTGACCGCATTTAGTGGCAGCGGCTGTGGACAG	247
Qy	287	attcacctcacccatacagcagctgtcgcagctggaagacgtgtgacatttatcttcagc	346
Db	248	ATTTCAGCTCACCACTCAGACAGACCTCGACGCTGAAAGATGTGGCACTTTATTTGTACG	307
Qy	347	aatcta--taattttacacgcttcgcagcagggagggaccaaagttygaataaaa	396
Db	308	AATATTATAGTACCTCCATCACTTCGGCCAAGGACACGACTGGAGTTAAA	360
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DEFINITION	UI-HF-BL0-aci-a-09-0-U1.r1 NIH_MGC_37 Homo sapiens CDNA clone		16-FEB-2000
ACCESSION	AM406512	IMAGE:3060017 5', mRNA sequence.	
VERSION	AM406512.1	GI:6925569	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 630) NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) On Jun 5, 1998 this sequence version replaced gi:3189280. Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/dbip/image/image.html Seq primer: M13 Forward.		
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		/cell_line="MGC85"	
		/lab_host="DH10B (LTR)"	
		/note="Vector: pUT73-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonafide, Ph.D. and M. Bento Soares, Ph.D."	
BASE COUNT	162 a	178 c	156 g
ORIGIN		134 t	
Query Match	56.7%	Score 224.6;	DB 72; Length 630;
Best Local Similarity	79.5%	Pred. NO. le-58;	
Matches 279:	Conservative	0; Mismatches	69; Indels
			3; Gaps
			1;

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 8 GGGGCTTAGGGGACATCGTGTGATGATGACCACTCTCCAGACTCCCTGGCTGTCTGTGGGC 67
 109 gagaaggccactattagctgcaaatccagtcagcagctgtgtcctacacagtagaacccagag 168
 68 GAGAGGGCCACCACTCAATGTCAGTCCAGCCAGCCAGTCTTTATACAGCTCCCAATTAAG 127
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 248 TTCACCTCACCATCAGCAGCGCTGCAAGGCGTAAGATGTGGCACTTATTACTCTCAGCAA 307
 349 tcttataatctt---tacacgttcggacaggggacccaaggtggaataaa 396
 308 TATTATAGTATTCCTTCACCTTCGGCCAGGACAGCAGACTCGAGATTAA 358
 RESULT 6
 AA06484 328 bp mRNA EST 16-FEB-2000
 LOCUS UI-HF-BL0-acr-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3060232 5', mRNA sequence.
 ACCESSION AA06484
 VERSION AA06484.1 GI:6925541
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 328)
 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M3 Forward.
 Location/Qualifiers
 1..328
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3060232"
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 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DHIOB (LTI)"
 /note="Vector: p7/T3-Pac; Site.1: NotI; Site.2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 78 a 92 c 84 g 74 t
 ORIGIN

Query Match 55.8%; Score 220.8; DB 72; Length 328;
 Best Local Similarity 81.7%; Pred. No. 1.3e-57;
 Matches 255; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 53 cctgtgggagacattgtgtcacacagctccacagatccctgtgtgctgaagcttaga 112
 8 CCAAGGGGACATCGTGTGATGATGACCACTCTCCAGACTCCCTGGCTGTCTGTGGGC 67
 113 gggcactattagctgcaaatccagtcagcagctgtgtcctacacagtagaacccagagact 172
 68 GGGCCACCACTCAATGTCAGTCCAGCCAGCCAGTCTTTATACAGCTCCCAATTAAGACT 127
 173 actgtgtgtgtacacagcagaacacagggcagcctctcctaactgtgtactgtg 232
 128 ACTTACTTGTGTTGTGTACACAGCAAGAAACGACAGCTCTCAAGCTGCATATTTCTG 187
 233 ccaataggaatctgtgtccctgtatcgtcttcagtcagtcagtcagtcagtcagtcag 292
 188 CTACCCGGGAAATCCGGGTCCTGTGACCGATTCAGTGTGAGCGGCTGTGGACAGATTCA 247
 293 ctccacacatcagcagctgtcagcagctgaaagcgtgtgcaatttactcagcagaact 352
 248 CTCTCACCATCAGCAGCGCTGCAAGGCGTAAGATGTGGCACTTATTACTCTCAGCAATAT 307
 353 ataacttaca 364
 308 ATAGTACTCTCA 319
 RESULT 7
 AA300651 363 bp mRNA EST 18-APR-1997
 LOCUS ESTr13764 Testis tumor Homo sapiens cDNA 5' end similar to similar
 DEFINITION to immunoglobulin light chain, V region, anti-IgD A, mRNA
 sequence.
 ACCESSION AA300651
 VERSION AA300651.1 GI:1953221
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 363)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle,Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,Y.-I., Marmas,S.M., Merrick,J.M.,
 Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Seudek,D.M., Shirley,R.,
 Small,R.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dime,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A.,
 He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 suppl.), 3-174 (1995)
 12140200
 Other ESTs: TNC102133
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression

SOURCE	ORGANISM
human.	Homo sapiens

KEYWORDS	EST.
SOURCE	human.

[illegible]

FEATURES	COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	REGION (HUMAN);	IMAGE:7/1198/15	EST	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
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						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.	AA0405415.1	GI:2063652	EST.	AA0405415	442 bp	RNA	09-Nov-1997	AA0405415	LOCUS	DEFINITION	RESULT 12	Db	
						human.													

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		1..442				
		/organism="Homo sapiens"				
		/db_xref="GDB:5942254"				
		/db_xref="taxon:9606"				
		/clone="IMAGE:741987"				
		/clone_lib="Soares ovary tumor NbHOT"				
		/sex="female"				
		/tissue_type="ovarian tumor"				
		/lab_host="DH10B (ampicillin resistant)"				
		/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAAGTGGAGCGCGCGGGTGTGTGTGTGTGTGTGT 3']"				
		double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Felina Boudado."				
BASE COUNT	90 a	120 c	114 g	118 t		
ORIGIN						
Query Match	48.0%;	Score 190.2;	DB 26;	Length 442;		
Best Local Similarity	71.8%;	Pred. No. 3.6e-48;				
Matches 278;	Conservative	0;	Mismatches 103;	Indels 6;	Gaps 2;	
Oy	13	gccacgggtctctatattctgtctgtctgtatagggtatctgtgcacctgtgtgggaactgtgtctg	72			
Db	33	gctcagctcttgggggctcttaatgcttcttgggtcttcttgatccagtgagggtatatttggag	92			
Oy	73	acacagctctccagatccctctgctgcttaagctttagagagagaaggagccactattagctgcgaa	132			
Db	93	actcagctccacacttctcccttgccttccctctcattcccttgagagacccggcctccattctctgcagg	152			
Oy	133	tcacgtcagagctctctcaacagatgaagaccgcagagaactactgtgtgtgtacagcag	192			
Db	153	tctactcagagcctcct---gctttagtaattgagataattatttggatgtgatatcgcag	209			
Oy	193	aaacaggcagccctcctaaactctgtactctactctgtggcatccactagggaactctggggtc	252			

Db 210 AAGCAGGAGGAGTCTCCACAGCTCCTGATCTATTGGGTTTAAACGGGCTCCGGGGTTC 269
Oy 253 cctgctgcttcagtgagtgatctggtgagacatttaccctaccatcagcgtctg 312
Db 270 CCTGACAGGTTGAGTGCGAGTGAGTGCACAGCATTTTACACTAAAATCGACAGAGTG 329
Oy 313 caggtgagacgctgagcttattactcagcgaatct---tataatcttaccgttc 369
Db 330 GAGGCTGAGAGTGTTGGGTTTATCAGTCATGCAGGCTCTACATCTCTCAGACTTTT 389
Oy 370 ggaacgggagaccaggtggaataaaa 396
Db 390 GGCCAGGGAGACCAAGCTGAGATCAAA 416

RESULT 13
AM406796 423 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BL0-acz-f-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3060998 5', mRNA sequence.
ACCESSION AM406796
VERSION AM406796.1 GI:6925853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jan 6, 2000 this sequence version replaced gi:6675816.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 forward
Location/Qualifiers
1. 423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3060998"
/clone_1id="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTR)"
/note="Vector: pTR73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafido, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 98 a 125 c 108 g 92 t
ORIGIN

Query Match 47.6%; Score 188.4; DB 72; Length 423;
Best Local Similarity 69.9%; Pred. No. 1.3e-47;
Matches 277; Conservative 0; Mismatches 101; Indels 18; Gaps 1;

Oy 1 atgagttacagagccaggttcttatatgctgctgctatggtgacccgtgag 60
Db 14 ATGAGAGCCCGCCAGCTCTCTCCCTCCGCTACTGCTGCCACATACCACTGGA 73
Oy 61 gacattgtctgacacagctccagattccctgctgtaagcttagagagagggccact 120

Db 74 GAATAGATGATGACGACAGTCTCCAGCCACCCTGTCTGTCTCCAGGGGAAAGACCCACC 133
Oy 121 attagctcaaatccagtcagagtcgtctcaacagtagaaccggagaaactactgct 180
Db 134 CTCTCTCCAGGGCCAGTCAGAGTGTGTAGCA-----ACTTAGCC 175
Oy 181 tggtaaccagaaacacagggcagcctcctaactgctgactactggtgacaccagtg 240
Db 176 TGGTACCAACAGAAACCTGGCCGGGCTCCAGGCTCTCACTATAGTGTACCAACGAG 235
Oy 241 gaattcgggtccctgacgtctcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
Db 236 GCCACTGTATCCCGATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 295
Oy 301 atcagcagctcgcagcgtgagacgtgagcttattactcagcgaatctataatctt 360
Db 296 ATCAGCAGCTGCACTGCAAGTCTGCAAGTCTGCAAGTCTGCAAGTCTGCAAGTCTGCAAG 355
Oy 361 tacacgttcgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
Db 356 CAAAGCTTGCCAGGAGCAGCAGGTGGAATCAAA 391

RESULT 14
AM405725 488 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BL0-abv-f-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057944 5', mRNA sequence.
ACCESSION AM405725
VERSION AM405725.1 GI:6924782
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Seq primer: M13 forward
Location/Qualifiers
1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057944"
/clone_1id="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTR)"
/note="Vector: pTR73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafido, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 105 a 129 c 129 g 125 t
ORIGIN

Query Match 46.0%; Score 182.2; DB 72; Length 488;
Best Local Similarity 72.0%; Pred. No. 1.1e-45;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2000, 06:25:32 ; Search time 72.06 Seconds

(without alignments)
1374.911 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattcaacagcagccaggt.....ggaccacagtggaataaaa 396

Scoring table: IDENTITY_NNC

Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues 623170

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	340	85.9	480	1	N91663	Light chain of mon
2	332	83.8	952	1	Q94036	Mab 55.1 light cha
3	301.4	76.1	439	1	T60729	CDNA encoding huma
4	301.4	76.1	439	1	T60730	CDNA encoding huma
5	298.2	75.3	399	1	Q66845	Sequence encoding
6	293.6	74.1	402	1	T43415	Xenograft antibody
7	288.6	72.9	399	1	Q74067	Monoclonal antibody
8	288.6	72.9	439	1	T60734	CDNA encoding wild
9	286.8	72.4	418	1	T34152	Monoclonal antibody
10	285.4	72.1	439	1	T72268	Chimeric Mab 15 PC
11	285.4	72.1	460	1	T72238	Mouse Mab 15 light
12	283.2	71.5	342	1	X34465	Chimeric Mab 6A4
13	279.8	70.7	1443	1	Q62958	Mouse Mab 6A4 light
14	277.8	70.2	747	1	V36237	Glycophorin antibo
15	275.8	69.6	870	1	O62956	DNA od ScFv D3M wh
16	275.2	69.5	660	1	O53430	Glycophorin antibo
17	270.6	68.3	330	1	V29839	Sequence encoding
18	270.6	68.3	864	1	V72072	Anti-DNA IL/TM (H2
19	270.6	68.3	2019	1	V72059	Fusion protein PIC
20	270.6	68.3	2025	1	V72064	Plasmid pMG4/55.1s
21	267.2	67.5	336	1	X34588	Fusion protein PNG
22	267.2	67.5	1701	1	O30919	Mouse Mab 6A4 muta
23	267.2	67.5	1701	1	O30920	PMR1006 insert. N
24	261.4	66.0	400	1	N80499	Vector pMDR1007. N
25	260.8	65.9	511	1	N80499	Encodes V region o
26	257.4	65.0	398	1	O66699	EST clone AY241. N
27	257.4	65.0	798	1	O34842	DRG-200 Ab light
28	250.2	63.2	407	1	O26047	Encodes V kappa reg
29	248.6	62.7	402	1	T00780	V-region of L-chain
30	248.6	62.7	402	1	T00780	E-selectin-specifi
31	247	62.4	5703	1	Q30900	Insert pMDR1003. N
32	247	62.4	5703	1	V03504	Anti-IL-5 humanise
33	241.6	61.0	336	1	Q30881	Plasmid pCNI15H2IC
						5A8 VL. New anti-C

34	241	60.9	340	1	Q30880	PMR927 insert. Ne
35	239.8	60.6	340	1	Q73232	Murine L chain fro
36	238.6	60.3	795	1	O04263	Encodes Colon can
37	238.2	60.2	342	1	Q23341	Murine kappa chain
38	238.2	60.2	342	1	Q74303	Mouse HmFcl light
39	237.8	60.1	1373	1	N80941	Encodes Vchi regio
40	236.6	59.7	339	1	O68710	Humanised Mab L-ch
41	236.6	59.7	340	1	O32776	Light chain variab
42	236.2	59.6	619	1	N80498	Encodes V region o
43	233.6	59.0	1479	1	X34596	DNA encoding a cm
44	233.4	58.9	339	1	Q44841	Mab NPS2 light cha
45	233.4	58.9	726	1	T18829	Single chain murin

ALIGNMENTS

RESULT 1
ID N91663
AC N91663: standard; DNA: 480 BP.
DI 14-MAR-1990 (first entry)
DE Light chain of monoclonal antibody 6A4.
KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
FH Key Location/Qualifiers
FT cds 37..480
FT /tag= a
FN EP-338395-A.
FD 25-OCT-1989.
PR 12-APR-1989; 106463.
PR 19-APR-1988; DE-813023.
PA (BEHM) Behringwerke.
PI Dondrey H, Marger M, von Specht BU.
DR WPI: 89-310861/43.
DR P-PSDB: P93078.
PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
PS variable antibody regions.
PS Claim 1: page 6: 7pp; german.
CC The sequence has a variable and constant region. Monoclonal antibody 6A4
CC reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa.
CC It is used for therapy and diagnosis of infection, and as a carrier for
CC drugs. The antibody is IgG2a subclass.
SQ Sequence 480 BP; 115 A; 118 C; 135 G; 112 T;

Query Match 85.9%; Score 340; DB 1; Length 480;
Best Local Similarity 91.2%; Pred. No. 1.4e-102;
Matches 361; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY	1	atgattcaacagcagccaggtctctattgtcgtcgtcatggtatcggaccctgtgg	60
DB	37	ATGGATTCAACAGCCAGGCTCTTATATGCTGCTGATGGTATCGTGGG	96
QY	61	gacattgtcgtacacagctccagattccctgtcgtgtaagttagagagagccact	120
DB	97	GACATTGTGATCTACAGCTCTCCTCCCTGCTGTGTACGACGAGAGAGTCACT	156
QY	121	attagctgcaaatccagtcagatcgtctcaacagtagaaccggagagaacttggct	180
DB	157	ATGACTGCAATCCAGTCAGTCAAGTCTGTCACACAGTATACCCGAAGAATCTTGCT	216
QY	181	tgttcacagcagaacacccagggagcgtctcctaactgcgtgattatcggacactgg	240
DB	217	TGTTACCAAGCAAAACCAAGGCGATCTCTTAACGCTGATTTACTGGCAACCACTAG	276
QY	241	gattcggagtcctccagtcagtcctcagtgagcagtgatcgtgacagattcactcacc	300
DB	277	GATCTGGGCTCCCTGATCCCTTACAGGCAATGATCTGGACGATTTCTCTCAC	336
QY	301	atcagcagtcctcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc	360
DB	337	ATCAGCAGTGTCAAGCAGTCAAGCAGTGTCTTACTGCAACCAATCTATATCTT	396

Db 268 GAATCTGGGTCCTGATCGCTTCAGTGGCAGTGCATGTGGAAACAGATTTCACCTCACC 327
 QY 301 atcagcagctctgcagcgttgaaagcgttgccattatctacgtcagcgaactctata---at 357
 Db 328 ATGAGCAGTGTGCGAGGTGAAGAGCTGGCACTTTATTACTGTCAAGATGATTATAGTTAT 387
 QY 358 cttaacagcttcgcagcagggagaccaggttgaaataaa 396
 Db 388 CCGCTCACGTTTCGTCAAGGACCAGGTGAGATMAAA 426

RESULT 4

T60730 standard: cDNA: 439 BP.
 ID T60730.
 AC T60730.
 DT 25-SEP-1997 (first entry)
 DE cDNA encoding humanised murine anti-E-selectin antibody CY1788V(LB).
 KW Humanised; murine; mouse; E-selectin; antibody; light chain;
 KW variable region; detection; inhibition; mediation; cell adhesion;
 KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
 KW acute respiratory distress syndrome; gross cystic breast disease;
 KW cancer; treatment; splanchic occlusion shock; psoriasis;
 KW complement; chimeric; ds.
 OS Chimeric - Mus spp.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 FH Key
 FT Location/Qualifiers
 FT 16..426
 FT cds /*tag- a
 /note- "no stop codon given"

WO9640942-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U09204.
 PR 07-JUN-1995; US-482112.
 PA (CYTE-) CYTEL CORP.
 PI Bendig KM, Jones ST, Perez C, Saldanha JW, Williams MA;
 PI Jones S;
 DR WPI: 97-07772/07.
 DR P-PSDB: W10545.
 PT Humanised anti-E-selectin antibody - useful for diagnosis and
 PT treatment of, e.g. inflammatory responses, septic shock, acute
 PT respiratory distress syndrome or cancer
 PS Claim 29: Page 71: 89pp: English.
 CC The present sequence encodes the humanised murine anti-E-selectin
 CC antibody (Ab) light chain variable region, CY1788V(LB). The Ab can
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell
 CC adhesion. It can also be used to diagnose, reduce or inhibit an
 CC inflammatory response, or the severity of pathologies, e.g. septic
 CC shock, acute respiratory distress syndrome, wound associated
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
 CC splanchic occlusion shock, or psoriasis. It can be administered to
 CC a human without inducing an immune response, in addition, the
 CC effector portion of the Ab can interact with various components of
 CC the human immune system, including complement.
 SQ Sequence 439 BP; 106 A; 110 C; 118 G; 105 T;

Query Match 76.1%; Score 301.4; DB 1; Length 439;
 Best Local Similarity 86.5%; Pred. No. 7e-90;
 Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
 QY 1 atgagctcaacagcagcaggtctctatatctgtctgtctatggatcttgacactgtggg 60
 Db 28 ATGAGAGTCACAGTTCAGGTCCATGTCCTGCTGTCTCTGGTATCTGATCACTGTGGG 87
 QY 61 gacattgtctgacacagctccagatccctgtgctgtaagcttagaggaagggccact 120
 Db 88 GACATTGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGGAAGGCCACC 147
 QY 121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactacttgct 180
 Db 148 ATCAACTGCAAGTCCAGTCAAGTCTGTACACAGTGAATCAAAAGAACTACTTGACC 207

QY 181 tgfaccacagcaaaaccagggcagcctctctaaactgtctgtacttggtgcatcactagg 240
 Db 208 TGTATACAGCAGAAACCAAGGACCTCTCCTAAGCTGTGATCTACTGTGGCATCCACTAGG 267
 QY 241 gaactgtggtccctgtactcgtcttcagtgagcagtgagatctggacagattcactcacc 300
 Db 268 GAATCTGGGTCCTGATTCGCTTCAAGTGGCAGTGTGAAACAGATTTCACCTCACC 327
 QY 301 atcagcagctctgcagcgttgaaagcgttgccattatctacgtcagcgaactctata---at 357
 Db 328 ATGAGCAGTGTGCGAGGTGAAGAGCTGGCACTTTATTACTGTCAAGATGATTATAGTTAT 387
 QY 358 cttaacagcttcgcagcagggagaccaggttgaaataaa 396
 Db 388 CCGCTCACGTTTCGTCAAGGACCAGGTGAGATMAAA 426

RESULT 5

066845 standard: DNA: 399 BP.
 ID 066845.
 AC 066845.
 DT 31-DEC-1994 (first entry)
 DE Sequence encoding the light chain variable region of the mouse NA-8
 DE antibody, including the signal sequence and mature chain.
 KW Antibody NA-8; human CD18; complementarity determining region; CDR;
 KW ss.
 OS Mus musculus.
 FH Key
 FT Location/Qualifiers
 FT 1..399
 FT cds /*tag- a
 /note- a
 WO9412214-A.
 PD 09-JUN-1994.
 PF 30-NOV-1993; U11611.
 PR 01-DEC-1992; US-983949.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Landolfi NF;
 DR WPI: 94-199973/24.
 DR P-PSDB: R59509.
 PT New humanised antibodies specific for CD18 - derived from new
 PT murine antibody NA-8, prevent binding of neutrophils to
 PT endothelial cells, useful for treating inflammation
 PS Disclosure: Fig 1A: 50pp: English.
 CC The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy
 CC chain and light chain variable domain genes of NA-8 were cloned
 CC using anchored PCR. The cDNA variable domain sequences and the
 CC deduced AA sequences are shown in 066845/R59509 and 066846/R59510.
 SQ Sequence 399 BP; 102 A; 88 C; 100 G; 109 T;

Query Match 75.3%; Score 298.2; DB 1; Length 399;
 Best Local Similarity 86.0%; Pred. No. 7.ee-89;
 Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;
 QY 1 atgagctcaacagcagcaggtctctatatctgtctgtctatggatcttgacactgtggg 60
 Db 1 ATGAGATTCACAGGCCAGGTCTTATGTTACTGTGCTGATGCTGATTCGAACTGTGGG 60
 QY 61 gacattgtctgacacagctccagatccctgtgctgtaagcttagaggaagggccact 120
 Db 61 GACATTGTGATGACACAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGGAAGGCCACTACT 120
 QY 121 attagctgcaaatccagctcagagctgtctcaacagtagaacccagagaaactacttgct 180
 Db 121 ATGAGCTGCAAGTCCAGTCAAGCCTTTATATATAGTATTCATTAAGAAATTAATCTGGCC 180
 QY 181 tgfaccacagcaaaaccagggcagcctctctaaactgtctgtactctgtggtatcactagg 240
 Db 181 TGTATACAGCAGAAACCAAGGACCTCTCCTAAGCTGTGATCTACTGTGGCATCCACTAGG 240
 QY 241 gaactgtggtccctgtactcgtcttcagtgagcagtgagatctggacagattcactcacc 300
 Db 241 GAATCTGGGTCCTGATTCGCTTCAAGTGGCAGTGTGAAACAGATTTCACCTCACC 300

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OY 301 accagcagctcgcagcctgaagacgttgagcttattactgacgcaatctata---at 357
    ||||||| || ||||||| ||||||| ||||||| ||||||| ||||||| ||
DB 301 ATCAGCAGTGTGAAGCTTAAGCACTGCGAGCTTATTACTGTCAGCAATATTATAGCTAT 360
OY 358 cttacacgttcgcagcaggagcgaagtggaataaaa 396
    | | ||||||| ||||||| ||||||| ||||||| ||||||| ||
DB 361 CCATTCAGCTGCTCGCGGACAAAGTTGGAATATAAA 399

RESULT 6
T43415 6
ID T43415 standard; cDNA to mRNA; 402 BP.
AC T43415;
DT 17-FEB-1997 (first entry)
DE Xenograft antibody HAR-1 light chain variable region cDNA.
KM animal model; hamster; monoclonal antibody; HAR-1; ds.
OS Rattus sp.
FH Key
FH cds
FT 1. .402 Location/Qualifiers
FT /product= immunoglobulin variable region
FT /standard_name= Ig kappa chain variable region
FT /label= VK_Region
FT /note= "HAR-1 kappa light chain variable region"
FT 1. .60
FT /tag= b
FT /standard_name= Leader
FT /label= Leader
FT 61. .129
FT /tag= c
FT /standard_name= Framework region 1
FT /label= FR-1
FT /note= "framework region 1 of HAR-1 kappa light
FT chain variable region"
FT 130. .180
FT /tag= d
FT /standard_name= CDR-1
FT /label= CDR-1
FT /note= "complementarity determining region 1 of
FT HAR-1 kappa light chain variable region"
FT 181. .225
FT /tag= e
FT /standard_name= Framework region 2
FT /label= FR-2
FT /note= "framework region 2 of HAR-1 kappa light
FT chain variable region"
FT 226. .246
FT /tag= f
FT /standard_name= CDR-2
FT /label= CDR-2
FT /note= "complementarity determining region 2 of
FT HAR-1 kappa light chain variable region"
FT 247. .342
FT /tag= g
FT /standard_name= Framework region 3
FT /label= FR-3
FT /note= "framework region 3 of HAR-1 kappa light
FT chain variable region"
FT 343. .366
FT /tag= h
FT /standard_name= CDR-3
FT /label= CDR-3
FT /note= "complementarity determining region 3 of
FT HAR-1 kappa light chain variable region"
FT 367. .402
FT /tag= i
FT /standard_name= Framework region 4
FT /label= FR-4
FT /note= "framework region 4 of HAR-1 kappa light
FT chain variable region"
FT
PN W09636358-A1.

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PD 21-NOV-1996.
PF 14-MAY-1996; U06804.
PR 15-MAY-1995; US-440621.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Cramer DV, Makowka L, Wu G;
DR WPI; 97-011852/01.
DR P-PSDB; W06206.
PT Inhibiting xenograft rejection by modifying antigen expression of
PT the graft - prevents binding of anti-donor antibody and prolongs
PT graft survival
PS Claim 10; Page 99; 135pp; English.
CC A cDNA clone (T43415) codes for the kappa light chain variable
CC region (W06205) of the LEW rat anti-hamster xenograft monoclonal
CC antibody HAR-1. It was obtd. from a HAR-1 light chain cDNA library
CC by PCR amplification (see also T43425-26) and can be used to
CC produce recombinant HAR-1 antibody fragments, e.g. Fab(')2 and
CC Fab. These block binding of preformed anti-donor xenograft
CC antibodies in a recipient animal serum to antigen expressed by
CC endothelial cells of the xenograft, i.e. they inhibit antibody-
CC mediated rejection, thereby prolonging the survival of the hamster
CC xenograft in a recipient.
SO Sequence 402 BP; 102 A; 99 C; 107 G; 94 T;

Query Match 74.1%; Score 293.6; DB 1; Length 402;
Best Local Similarity 83.8%; Pred. No. 2.5e-87;
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

OY 1 atggaattacagggcccaggtcttatattgctgctcatggtatcgcacctgtgg 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 ATGGATATCACAGACACAGAGTCCCTCATGTCCCTGCTGCTGGATVTCGTACCTGTGG 60
OY 61 gacattgctgcagcacagctccagatccctgctgctgtaagcttagggagagggccact 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 GACATTGTGATGATACCCCAACTCTCATCTCCAGGCTGTGTAGCAGGGAAGAGTCACT 120
OY 121 attagctgcaaatccagtcagagctgtgtctcaacagtagaaccgagagaactactgtgct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 ATGACCTGCAAGTCCAGTCAGAGCTCTTTATATACATGAAACAAAAGAACTACTGTGCC 180
OY 181 tggctccagcagaacccaagggcagcctctcctaactgtcatctctctggtgcatcactagg 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 TGGTACCGGCGAAGAACCGAGGGCAGTCTCTTAACGTGATCTACTGGGCATCCACTAGG 240
OY 241 gaattctgggtccctgagctgcgttcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 GAATCTGGGGTCCCTGATGCGCTTCAATAGGCAATGAGATCTGGGACAGATTACTGTGACC 300
OY 301 atcagcagctcgcagcctgaagacgttgagcttattactgacgcaatctataatctt 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 ATCAGCAGTGTGAAGCTTAAGCACTGCGAGCTTATTACTGTCAGCAATATTATAGCTAT 360
OY 361 taccagcttcgcagcaggagcgaagtggaataaaa 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 361 TACAGCTTGTGAGCTGCGGACCAAGCTGGAAGTGAAGTGA 396

RESULT 7
O74067 7
ID O74067 standard; DNA; 399 BP.
AC O74067;
DT 02-JUL-1996 (first entry)
DE Monoclonal antibody; CB-Hep 1, light chain variable domain cDNA.
KM HBV, hepatitis B virus surface antigen; monoclonal; antibody;
KM CB-Hep 1; Immunopurification; detection; hybridoma; recombinant; Fv;
KM variable; VH; HBSAg; ss.
OS Mus sp.
FH Key
FH cds
FH location/Qualifiers
FT 1. .399
FT /tag= a
FT signal_peptide 1. .60
FT /tag= b
FT mat_peptide -61. .399

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FT		/tab- c	61..129	
FT	misc_feature	/*tag= d		
FT		/label= FR1	130..180	
FT	misc_feature	/*tag= e		
FT		/label= CDR1	181..225	
FT	misc_feature	/*tag= f		
FT		/label= FR2	226..246	
FT	misc_feature	/*tag= g		
FT		/label= CDR2	247..342	
FT	misc_feature	/*tag= h		
FT		/label= FR3	343..369	
FT	misc_feature	/*tag= i		
FT		/label= CDR3	370..399	
FT	misc_feature	/*tag= j		
FT		/label= FR4		
PN	EP-686696-A1.			
PD	13-DEC-1995.			
PF	09-JUN-1995; 201535.			
PR	09-JUN-1994; CU-000073.			
PA	(ING-) CENT ING GENETICA & BIOTECNOLOGIA.			
PI	(KAMB-) KAMBEEL R W.			
PI	Ayala Avila MA, Caraan-Haden Frias IM; del Carmen Dominguez Horta MC;			
PI	Fernandez de Cossio Dorta-Duque ME, Gavilondo Cowley JVG;			
DR	WPI: 96-021914/03.			
DR	P-PDB: R85909.			
PT	New recombinant single chain Fv antibody fragment - useful for			
PT	Immuno.purificn. and detection of HBsAg			
PS	Claim 1; Page 19; 23Pg; English.			
CC	Q74066 and Q74067 encode the heavy and light chain variable domains of			
CC	The murine hybridoma-derived monoclonal antibody CH-Hep.1 Fv region.			
CC	The heavy and light chain regions are used to produce a recombinant			
CC	antibody fragment having specificity for the hepatitis B virus			
CC	surface antigen (HBsAg). The recombinant antibody may be used for			
CC	immunopurification of HBsAg, in immunoassays for the detection of			
CC	HBsAg and for insolubilisation of heterologous fusion proteins			
SQ	expressed in E. coli aiding their purification.			
	Sequence 399 BP; 98 A; 88 C; 101 G; 112 T;			
<hr/>				
Query Match 72.9%; Score 288.6; DB 1; Length 399;				
Best Local Similarity 84.5%; Pred. No. 1,1e-85;				
Matches 337; Conservative 0; Mismatches 39; Indels 3; Gaps 1				
OY	1 atgattaccagagccaggcttcttatatgtcgcgtgactagtgtatctggacacctgtgg 60			
Db	1 ATGGATTACCAAGGCCCAGGTTCTTATNGTTACTGCCTGTCTATGGTAGTCGTACTGTGGG 60			
OY	61 gacatttgctgacacagcttcacagattccctgctgtgaagcttagagagagggccact 120			
Db	61 GACATTGTGATGTCCACAGCTCTCACCTCCATCGTGCTGTCAGTTGTGAAGAAGGTTGCT 120			
OY	121 attacttccaataacagttagagttctgtgcccaacagtaagaaccggagaaactacttgct 180			
Db	121 TTGAGCTCTCAAGTCCAGTGTAGAGATCTTTATATCTTAACAATAACACAAAGAACCTTAGTGGCC 180			
OY	181 tggatcccgacgaacacccagagcagcctccctaactgcatctactctggcactcactagg 240			
Db	181 TGGTTCACGACCAAAACCTGGGCAAGTCTCTTAACATCTCATTTTACGGGCATCCACTAAG 240			
OY	241 gaactgggggtccctgatctgccttcagtgtgagcagtygtgacitgyggacagatttcaactcac 300			
Db	241 GATCTGGGGGTCCCGATGATGCTTTCACAGCAGCAGNGATGTGGGCAAGATTTCACCTGCANG 300			
OY	301 atcagcagctgcacagctgaaagacgtggagctttatatctatgcacgcaactcata---at 357			
Db	301 ATTCACAGTGTAAAGCTGTAAAGACCCTGGCGAGTTTATTTACTGTCAACAATATTAATTAAT 360			

ID	Accession	Score	DB	Length	Query Match
358	cttiacagttcggacaggggagccaaagttggaataaaaa	396			
361	ccgtacacgttcggagggggacacaaagctgcaaaatmaa	399			
RESULT	8				
ID	T60734	standard; cDNA; 439 BP.			
AC	T60734.1				
DT	25-SEP-1997	(first entry)			
DE	cDNA encoding wild type murine anti-E-selectin antibody CY187V(L).				
KE	Humanised; murine; mouse; E-selectin; antibody; light chain;				
KM	variable region; detection; inhibition; mediation; cell adhesion;				
KW	diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;				
KM	acute respiratory distress syndrome; gross cystic breast disease;				
KM	cancer; treatment; splanchnic occlusion shock; psoriasis;				
KM	complement; ds.				
OS	Mus spp.				
FT	Key	Location/Qualifiers			
FT	cds	16..426			
FT		/tag= "a			
FT		/note= "no stop codon given"			
PN	W09640942-A1.				
PD	19-DEC-1996.				
PF	06-JUN-1996; U09204.				
PR	07-JUN-1995; U5-482112.				
PA	(CYTE-) CYTEL CORP.				
PI	Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;				
PI	Jones S;				
DR	WPI; 97-077272/07.				
DR	P-PDB; W10547.				
PT	Humanised anti-E-selectin antibody - useful for diagnosis and				
PT	treatment of e.g. inflammatory responses, septic shock, acute				
PT	respiratory distress syndrome or cancer				
PS	Example 11; Page 55; 89pp; English.				
CC	The present sequence encodes the wild type murine anti-E-selectin				
CC	antibody (Ab) light chain variable region, CY187V(L), which was				
CC	used in the preparation of the humanised anti-E-selectin Ab light				
CC	chain variable regions, CY188V(LA-B). The humanised Ab can				
CC	be used to detect E-selectin, or inhibit E-selectin mediated cell				
CC	adhesion. They can also be used to diagnose, reduce or inhibit an				
CC	inflammatory response, or the severity of pathologies, e.g. septic				
CC	shock, acute respiratory distress syndrome, wound associated				
CC	sepsis, gross cystic breast disease or cancer, or treat, e.g.				
CC	splanchnic occlusion shock, or psoriasis. They can be administered				
CC	to a human without inducing an immune response. In addition, the				
CC	effector portion of the Ab can interact with various components of				
CC	the human immune system, including complement.				
SQ	Sequence 439 BP; 108 A; 110 C; 116 G; 105 T;				
Query Match	72.9%; Score 288.6; DB 1; Length 439;				
Best Local Similarity	84.5%; Pred. No. 1.1e-85;				
Matches 337; Conservative	0; Mismatches 59; Indels 3; Gaps 1;				
1	atgagttaacagggccaggctctctattatgtcgcgcgcgcattggtatctcgaccctgtgg	60			
28	atggagttcacaacacacgtcctcctcctcctcctcctcctcctcctcctcctcctcctcct	87			
61	gacattgtactacacacgtcctcctcctcctcctcctcctcctcctcctcctcctcctcct	120			
88	gacattgtgattacacacacgtcctcctcctcctcctcctcctcctcctcctcctcctcctcct	147			
121	atgactgtcaaatccagtcagatcgtcgtcctcctcctcctcctcctcctcctcctcctcct	180			
148	atgactgtcgaatccagtcagatcgtcgtcctcctcctcctcctcctcctcctcctcctcct	207			
181	tgtgtccagcagaacacccagggcagcctcctcctcctcctcctcctcctcctcctcctcct	240			
208	tgtgtccagcagaacacccagggcagcctcctcctcctcctcctcctcctcctcctcctcct	267			
241	gaattcgtggtcccgatcgtcctcctcctcctcctcctcctcctcctcctcctcctcctcct	300			

```
Db 268 GAATCTGGGGTCCCTGATGCTTCACAGGAGTGAATCTGGAACAGATTCTACTCTCACC 327
      |||
Qy 301 atcagcagctctcagcagctcgaagcgtgagcagttattactcgcagcaatctata---at 357
      |||
Db 328 ATCAGCAGCTCTGAGAGCTGGAAGACCTGGCAGTTATTACTGTGAGATGATATTAGTTAA 387
      |||
Qy 358 cttacacgtctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
      |||
Db 388 CCGCTCACGTTCCGCTGCTGGGACCAAGGTGGAGCTGAAA 426
      |||

RESULT 9
ID T34152 standard; DNA; 418 BP.
AC T34152;
DE 14-FEB-1997 (first entry)
DI Monoclonal antibody PA1-3F10 variable light chain-encoding DNA.
KW PA1-3F10; antibody; hybridoma; LMBP1322CB; cancer; target; epitope;
KM killing; colorectal; lung; ovary; cytotoxin; neoplasia; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 2..418
FT /note= "no start or stop codon"
PD MO9622310-A1.
PE 15-JAN-1996; SE0029.
PR 18-JAN-1995; SE-000148.
PA (BIOI-) BIOINVENT INT AB.
PI Carlsson R, Jansson B;
DR WPI: 96-354478/35.
DR P-PSDB: R99469.
PT Monoclonal antibody PA1-3F10 produced by hybridoma BCM LMBP1322CB -
PT useful to target cancer cells for killing or detection
PS Claim 10; Fig 10; 62pp; English.
CC T34152 encodes the variable light (VL) chain of monoclonal antibody
CC PA1-3F10 produced by hybridoma BCM LMBP1322CB. The antibody is
CC directed against an epitope present on cancer cells. In particular
CC breast, ovary, lung and colorectal cancer cells. The antibody is
CC useful for detecting cancer cell epitopes and hence in the diagnosis
CC of cancer. The antibody can be conjugated to a cytotoxic compound and
CC targeted to cancer cells to kill them.
SQ Sequence 418 BP; 102 A; 100 C; 107 G; 109 T;

Query Match 72.4%; Score 286.8; DB 1; Length 418;
Best Local Similarity 84.8%; Pred. No. 4.4e-85;
Matches 334; Conservative 0; Mismatches 57; Indels 3; Gaps 1;
```

```
Qy 363 cacgttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 396
      |||
Db 361 GACGTTCCGCTGAGAGCACCAGCCTGGAATCAAA 394
      |||

RESULT 10
ID T72268 standard; cDNA; 439 BP.
AC T72268;
DE 03-JAN-1998 (first entry)
DI Chimeric MAb 15 PCR-modified light chain variable region cDNA.
KW Humanised antibody; monoclonal antibody; MAb 15; tumour;
KM lung cancer; therapy; ds.
OS Chimeric mus musculus.
FH Key Location/Qualifiers
FT sig_peptide 16..87
FT /tag= a
FT mat_peptide 88..1426
FT /tag= b
PD EP-781847-A1.
PE 02-JUL-1997.
PE 25-OCT-1996; 117154.
PR 06-NOV-1995; EP-117407.
PA (MERE) MERCK PATENT GMBH.
PI Bendig M, Jones T, Saldana J;
DR WPI: 97-334904/31.
DR P-PSDB: W21655.
PT Humanised form of murine monoclonal antibody MAb 15 - useful for
PT treating lung cancer;
PT Disclosure; Fig 4; 71pp; English.
CC This cDNA sequence comprises the light chain variable region VL
CC sequence of murine monoclonal antibody (MAb) 15 (DSM ACC2117),
CC modified for the expression of chimeric 15 antibody. The 5' and
CC 3' ends of the VL sequence (see also T72238) were modified by
CC PCR (see T72243-44) to provide a kozak sequence for efficient
CC translation, a 5' HindIII site for cloning into HCV vectors, a
CC 3' splice donor site at the J-C junction for splicing the mouse
CC variable regions to human constant regions and a 3' BamHI site for
CC cloning into HCV vectors. The VH sequence was similarly modified
CC (see T72269). The modified VL and VH sequences were used in a
CC claimed process to model and design novel humanised, reshaped MAb
CC 15 having humanised, reshaped VL and VH sequences (see W21651 and
CC W21652), which can be used for treating tumours, especially lung
CC cancer, and for the manufacture of a drug related to tumours,
CC especially lung cancer.
SQ Sequence 439 BP; 109 A; 107 C; 112 G; 111 T;

Query Match 72.1%; Score 285.4; DB 1; Length 439;
Best Local Similarity 84.0%; Pred. No. 1.3e-84;
Matches 335; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
```

QY	301	atccagcctcgcgaagcgcgaagcgttcttactgcagccatctatc---	at	357
Db	328	ATCAGCAGCGTGAAGGCTGAGAGACCCGGCAGTTTATTACTGTCACCATATTTCTAAGTAT		387
QY	358	cttaccagcttcgcagcagggaccacaaaggttggaataaa	396	
Db	388	CCTCGAGCTTCGGTGGAGGACCAAGCTGGAATCAAA	426	
RESULT	11			
TT72238				
AC	TT72238	standard; cDNA; 460 BP.		
DT	03-JAN-1998	(first entry)		
DE	Mouse MAB 15 light chain variable region cDNA.			
KW	Humanised antibody; monoclonal antibody; MAb 15; tumour;			
OS	Lung cancer; therapy; ds.			
OS	Mus musculus.			
FT	Key	Location/Qualifiers		
FT	sig_peptide	1..72		
FT	mat_peptide	*/tag= a		
FT		73..411		
FT		/*tag= b		
PN	EP-781847-A1.			
PD	02-JUL-1997.			
PF	25-OCT-1996; 117154.			
PR	06-NOV-1995; EP-117407.			
PA	(MERE) MERCK PATENT GMBH.			
PI	Bendig M, Jones T, Saldana J;			
PI	WPI: 97-334904/31.			
DR	P-PSDB: W21653.			
PT	Humanised form of murine monoclonal antibody MAb 15 - useful for			
PT	treating lung cancer			
PS	Claim 14; Fig 1; 71pp; English.			
CC	This cDNA sequence encodes the light chain variable region VL			
CC	(W21653) of murine monoclonal antibody (MAb) 15 (DSM ACC2117),			
CC	a MAb that shows a therapeutic effect on human tumour cells,			
CC	especially human lung cancer. The clone was isolated from			
CC	hybridoma cDNA using a degenerate leader sequence primer (T72233)			
CC	and a kappa constant region reverse primer (T72240). The VH region			
CC	(see T72267) was also amplified. The VL and VH sequences were			
CC	used in a claimed process for the production of novel humanised,			
CC	reshaped MAb 15 having humanised, reshaped VL and VH sequences			
CC	(see W21651 and W21652), which can be used for treating tumours,			
CC	especially lung cancer, and for the manufacture of a drug related			
CC	to tumours, especially lung cancer.			
SO	Sequence 460 BP; 112 A; 118 C; 113 G; 117 T;			
Query Match	72.1%; Score 285.4; DB 1; Length 460;			
Best Local Similarity	84.0%; Pred. No. 1.3e-84;			
Matches	335; Conservative 0; Mismatches 61; Indels 3; Gaps 1;			
QY	1	atggaattcagcagccaggttcttatatctgctcgtcatggtatctgcacactgtgg	60	
Db	13	ATGAGTCACATTCCTCGTCTTATGTACTGCTGCTAGTGATCTGTCACCTGTGG	72	
QY	61	gacatctgctgcagcagcttccaaattccctcgctgtaagcttggaagagggccact	120	
Db	73	GACATTGTGATCTCACAGCTCTCATCTCTCCCTAGCTGTCTCAGTTGGAGAGAGT	132	
QY	121	attagctcaaatcagtaagtagctctgctcaacagtagaacccggagagaactctggt	180	
Db	133	ATGAGCTGCAAGTCAGTCAGAGCCTTTTATATAGTAGCAATCAAAAGACTACTTGGCC	192	
QY	181	tgtgtccagcagaaaccagcagcgactccctaaactgctatctactggtggcatccactag	240	
Db	193	TGGTCCAGAGAAACCAAGGCGCAGTCTCTTAACAGCTGATTACTGGGCATCACTAG	252	
QY	241	gaattctgggtctcccgatctgctagtgtgcaatgtatctgggaacagattactctcacc	300	
Db	253	GAATCTGGGGTCTCCGATGCTTTCACAGGCACTGATGTGGAGACAGATTACTCTCACC	312	

```

Oy 301 ataccagcttcgagagcggaagagctggcactttatctctcagcgaactctata---at 357
Db 313 ATCAGCAGCGTGAAGGCTGAAGAAGCCCGGCACTTTATCTCTCAGCAAGATATCTACTAT 372
Oy 358 cttaacgcttcgcagcaggcgacccaaggtgggaataa 396
Db 373 CCTCGAGCTTCGGTGGAGCGCACCAAGCTGGAATCAAA 411

RESULT 12
ID X34465
AC X34465:
DT 25-JUN-1999 (first entry)
DE Mouse MAb 6A4 light chain variable region encoding DNA.
KW Rolling template; nucleic acid synthesis; polynucleotide polymerase;
RV gene production; primer; monoclonal antibody; 6A4; ss.
OS Mus sp.
PN M09914370-A1.
PD 25-MAR-1999.
PF 15-SEP-1998; U19157.
PR 15-SEP-1997; US-929856.
PA (HIAT// ROSE F D.
PI Hiatt AC, Rose FD;
WP: 99-244045/20.
DR P-PSDB: Y06830.
PT Producing specific polynucleotides using rolling templates
PS Example 6, Page 40; 109BP; English.
CC The invention relates to a method for producing polynucleotides having a
CC defined sequence using rolling templates that successively add
CC nucleotides (nts) to a longer primer strand. The method comprises: (1)
CC incubating, under annealing conditions, a primer and a template that has
CC a 5'-region not complementary to the primer, a 3'-region complementary to
CC the 3'-end of primer and a non-reactive 3'-terminus, with the template
CC being shorter than the primer; (1i) reacting the primer with at least one
CC in presence of a template-dependent polynucleotide polymerase to
CC extend it by at least one nt (complementary to the 5'-region of template)
CC at its 3'-end; (1ii) separating the template and the extended primer; and
CC (1v) repeating the cycle of (1)-(1ii) as often as needed to synthesize
CC the desired polynucleotide. The method is especially used to produce
CC genes or their segments. The method provides fast, accurate, inexpensive
CC synthesis of RNA or DNA and is more efficient than chemical coupling
CC processes. It has higher specificity and eliminates the need for
CC deprotection. The products can be cloned directly. The method avoids
CC problems of waste disposal and includes an inherent editing effect
CC (failure sequences will not be extended further in subsequent rounds) so
CC that purification of the end product is facilitated. Synthesis may take
CC place on a vector, simplifying cloning and sequences with codon usage
CC optimized for a particular host can be prepared. This represents the
CC nucleotide sequence of the light chain variable region of the mouse
CC monoclonal antibody (Mab) 6A4, synthesised by the method of the
CC invention.
SQ Sequence 342 BP; 88 A; 87 C; 87 G; 80 T;

Query Match 71.5%; Score 283.2; DB 1; Length 342;
Best Local Similarity 90.2%; Pred. No. 6,1e-84;
Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Oy 61 gacatttgcttacacaatctccagatccctcggtgtgaagcttagagagagggcact 120
Db 1 GACATTGTGATGTCACAGTCTCCATCCCTCCGCTGTGTCTCAGCAGGAGAGAGGTCTACT 60

Oy 121 attagctgcnaatccagtcagatcgtctcaacagtagaaccgcgagagaactacttgct 180
Db 61 ATGACCTGCAAAATCCAGTCAGAGTCTGCTCAACAGTATAACCCGAAAGAACTTGTGCT 120

Oy 181 tggctccagcagaaaccgcggcgagcctctctaactgcgtgacttatctggcatccactgg 240
Db 121 TGGTACCGACGCAAAACCGAGGCGCAGTCTCTTAACCTGCTGATCTACTGGGCACTCCAGT 180

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QY 241 gaatctgggggtccctgacgtcttcagtgagtgagtcggagacattcactccacc 300
DB 181 GAATCTGGGGGTCCCTGACGTCTTCACAGCCAGTGGAGTCGATCTCCTCAC 240
QY 301 atcagcaagctctgcaagcgttgaaagcgttgagcagtttacttgacgcaaatctatactt 360
DB 241 ATCAGCAGTGTGACAGGCTGAGACCTGGCAGTTTACTTACGACGAATCTTATATCTT 300
QY 361 tacacgtctcgacacaggggacccaaggttgaaataaaa 396
DB 301 CGACGCTTGGTGGAGGACCAAGCTGAAATCAAA 336

RESULT 13

Q62958
ID 062958 standard; DNA: 1443 BP.
AC 062958:
DT 09-SEP-1994 (first entry)
DE Glycophorin antibody 1C3 Fab coding region.
KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;
KW polymerase chain reaction; primer; antibody engineering;
KW humanized antibody; phagemid pHFA; plasmid p569;ss.
OS Synthetic.
PN WO9407921-A.
PM 14-APR-1994.
PF 24-SEP-1993: AU00491.
PR 25-SEP-1992: AU00491.
PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lah M, Malbyrl, Power BE;
DR WPI: 94-135515/16.
PT New target-binding polypeptide(s) used for diagnosis, etc. -
PT having a stable core polypeptide region with at least one
PT target-binding region covalently attached, opt. mutated to alter
PT specificity, etc.
PS Disclosure: Page 42; 67pp; English.
CC PCR primers given in Q62951-52 were used to clone anti-glycophorin
CC antibody 1C3 Fab coding region. The DNA sequence of the first 1443
CC bases of the Fab fragment in pHFA, ready for ligation post PCR
CC amplification for ligation into p569, is given in Q62958.
SQ Sequence 1443 BP; 391 A; 388 C; 351 G; 313 T;

Query Match 70.7%; Score 279.8; DB 1; Length 1443;
Best Local Similarity 84.6%; Pred. No. 14e-82;
Matches 314; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 26 tatgtctgtctatggtatctggtacactgttgagacattgtctgacagctccag 85
DB 734 TCTTACCGTTACTGTTTACCCCGGTAAACCAAGCCGATCTGTCACAGTCCAT 793
QY 86 attccctgctctaaagcttagagagaagggccactattgctgcaaatccagtcagatc 145
DB 794 CCTCCCTGCTGTGTCAGTAGAGAGAACGTCACTATGAGCTGCAGATCAGACAGTC 853
QY 146 ttgtctcaagtagaaccgaagaagaactacttgctgtgaccaagcgaagaacgaagcagc 205
DB 854 TGTTCACAGTAGAACCCCAAGAACTACTGTGACTGTGACACGCAAGAAACCAAGGCACT 913
QY 206 ctctcaaatctgcatctactggtcagcaccctagtaggaatctgggtccctgacgtctca 265
DB 914 CTCCTAAACCGGTGATCTACTGGGCATCACTAAGGAATCTGGGGTCCCTGATCGCTTCA 973
QY 266 gtggcagctggtacctggagacagattcaactcacaacacagcagctgcaagctgaagacg 325
DB 974 CAGGCGTGGATCTGGAGACAGATTCTACCTCACCATCAGCAGTGTGACGGCTGAGAGACC 1033
QY 326 ttggcagtttactactgacagcaaatctataatcttaacagtttcgagcaggggagcaag 385
DB 1034 TGGCAGATTATTAAGTCAAGCAATCTTATATCTTGGAGCTTGGTGGAGGACCAAGC 1093
QY 386 tggaaataaaa 396
|||||

DB 1094 TGAATTTAA 1104

RESULT 14

V36237
ID V36237 standard; DNA: 747 BP.
AC V36237:
DT 08-SEP-1998 (first entry)
DE DNA od ScFv D3M which binds to mutant p53 proteins.
KW Single chain antibody; ScFv D3M; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment;
KW hyper-proliferation; cancer; re-stenosis; ss.
OS Mus SP.
PN WO9818625-A1.
PM 07-MAY-1998.
PF 27-OCT-1997: F01921.
PR 29-OCT-1996; FR-013176.
PA (RHON) RHONE-POULENC RORER SA.
PI Debussche L, Bracco L;
DR WPI: 96-272140/24.
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the
PT mutant, particularly for treatment of tumours
PS Claim 5; Page 32; 54pp; French.
CC The present sequence encodes a single chain antibody (ScFv) designated
CC D3M. The antibody binds to an epitope present in the C-terminal region
CC of the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv D3M is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv D3M is specific for
CC p53-mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
CC and to purify or detect p53.
SQ Sequence 747 BP; 189 A; 188 C; 205 G; 165 T;

Query Match 70.2%; Score 277.8; DB 1; Length 747;
Best Local Similarity 89.0%; Pred. No. 5e-82;
Matches 300; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 60 ggaactgtgtctgacacagctccagatccctggtctgtaagcttagagagaagggccac 119
DB 411 GGACATTGAGTGCACCCAGTCTCCATCTTCCCTGCTGTGACAGAGAGAGAGGTGCG 470
QY 120 tattagctgcaaatccagtcagagctctctcaacagtgaaacccgagaagactacttggc 179
DB 471 TATGAGCTGCAAAATCACTCAAGTCTTTCAACAGTAGAACCCGAAATTTACTTGGC 530
QY 180 ttgtgacacagcaagaacgaagcagccctcaaatgtgtgacttactggtgcatccagtag 239
DB 531 TTGATATACGCAAGAAACAGGCACTCTCTTAAGTGTGTGATCTCTGGCATCCACTAG 590
QY 240 ggaactgtggtccctgtactgcttcagtggtcagtgatctggagacagattcactctcac 299
DB 591 GGAATCTGGAGTCCCTGATTCGCTTCACAGGCGATGTGGAGATTCGACACTCTCAC 650
QY 300 catcagcagctctgcaagctgaaagcgtgagcagtttacttactgcaacgaattataact 359
DB 651 CATCAGCAGTGTGCAAGGCTGAAAGACCTGGCAGTTTATTAACGCAAGCAATCTTAAATCT 710
QY 360 ttacacgttcggaacaggggacccaaggttgaaataaaa 396
DB 711 ACCGACGTTTCGGCGGGGACCAAGCTGGAATCAAA 747
RESULT 15
Q62956

ID 062956 standard; DNA; 870 BP.
AC 062956;
DT 09-SEP-1994 (first entry)
DE Glycophorin antibody 1C3 scfv.
KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;
polymerase chain reaction; primer; scfv; single chain antibody;
phagemid pHEA; vector; antibody engineering; humanized antibody;
ss.
OS Not specified.
PN WO9407921-A.
PD 14-APR-1994.
PF 24-SEP-1993; AU0491.
PR 25-SEP-1992; AU-004973.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;
PI Lab M, Malbyrl, Power BE;
PI WPI: 94-135515/16.
DR P-PSDB; R52864.
PT New target-binding polypeptide(s) used for diagnosis, etc.
PT having a stable core polypeptide region with at least one
PT target-binding region covalently attached, opt. mutated to alter
PT specificity, etc.
PS Disclosure, Page 40; 67pp; English.
CC PCR primers N2034 (062947) and N2035 (062948) were used with anti-
CC glycophorin 1C3 antibody template DNA in a PCR to produce a 1C3
CC product of 3'-VH sequence juxtaposed to 5'-VL sequence flanked by
CC BstEII and NotI sites. Products were ligated with vector pHEA
CC containing a 1C3 scfv sequence, and expressed in Escherichia coli
CC TG1. The DNA sequence of the linkerless 1C3 scfv in pHEA is given
CC in 062956 (encoding protein R52864).
SQ Sequence 870 BP; 236 A; 205 C; 226 G; 203 T;

Query Match 69.6%; Score 275.8; DB 1; Length 870;
Best Local Similarity 89.0%; Pred. No. 2.4e-81;
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 61 gacatgtgctgcacacacatccagatccctgctgtaagcttagagagagggccact 120
DB 463 GACATGCGTCATGTCACATGTCATCCCTCGCTGTCTCAGTAGAGAGAGTCACT 522
QY 121 attagctgcaaatccagtcagatgctgtctcaacagtagaacccgagagaactactgct 180
DB 523 ATGAGCTGCAAGATCCAGTCAGTCTTCAACAGTAGAACCCGAAAGAACTACTGACT 582
QY 181 tggtaaccagcgaacccagggcagctcttaactgctgactactggtgcatcactagg 240
DB 583 TGGTACCGACGAGAAACAGGGCAGTCTCTAAACCGATCTACTGGGCACTCCACTAGG 642
QY 241 gaactgggggtccctgcatgcttcagtgagtgagtgagagagatttcaactcacc 300
DB 643 GAATCTGGGGTCCCTGATCGCTTCACAGGCACTGGGACAGATTTCACCTCTACC 702
QY 301 atcagcagctcgcagagctgaaagctgagcttatattactgacgcgaactctataactt 360
DB 703 ATCAGCAGTGTGCAAGGCTGGAAGACCTGCGAGATATATCTGCAAGCAATCTTAATCTT 762
QY 361 tacacgttcggagcaggagaccagaagtggaaataa 395
DB 763 CGGACGTTCGCTGGAGGACCAAGCTGGAATAATTA 797

Search completed: August 27, 2000, 06:25:36
Job time: 1933 sec

Query Match	70.7%;	Score 279.8;	DB 3;	Length 1443
Best Local Similarity	84.6%;	Pred. No. 7.4e-81;		

1
 2 ZIP: 94103
 3
 4 COMPUTER READABLE FORM:
 5
 6 MEDIUM TYPE: Floppy disk
 7
 8 COMPUTER: IBM PC compatible
 9
 10 OPERATING SYSTEM: PC-DOS/MS-DOS
 11
 12 SOFTWARE: PatentIn Release #1.0, Version #1.25
 13
 14 CURRENT APPLICATION DATA:
 15
 16 APPLICATION NUMBER: PCT/US93/11611
 17
 18 FILING DATE: 30-NOV-1993
 19
 20 CLASSIFICATION:
 21
 22 PRIOR APPLICATION DATA:
 23
 24 APPLICATION NUMBER: US 07/983,949
 25
 26 FILING DATE: 01-DEC-1992
 27
 28 ATTORNEY/AGENT INFORMATION:
 29
 30 NAME: Smith, William M.
 31
 32 REGISTRATION NUMBER: 30,223
 33
 34 REFERENCE/DOCKET NUMBER: 11823-45
 35
 36 TELECOMMUNICATION INFORMATION:
 37
 38 TELEPHONE: 415-326-2400
 39
 40 TELEFAX: 415-326-2422
 41
 42 INFORMATION FOR SEQ ID NO: 1:
 43
 44 SEQUENCE CHARACTERISTICS:
 45
 46 LENGTH: 399 base pairs
 47
 48 TYPE: nucleic acid
 49
 50 STRANDEDNESS: single
 51
 52 TOPOLOGY: linear
 53
 54 MOLECULE TYPE: CDNA
 55
 56 FEATURE:

;	NAME/KEY:	CDS
;	LOCATION:	1..399
PCT-US93-11611-1		

Query Match	70.1%;	Score 277.4;	DB 6;	Length 399;
Best Local Similarity	82.7%;	Pred. No. 2.6e-80;		
Matches 330; Conservative	0;	Mismatches 66;	Indels 3;	Gaps 1

QY	1	atggattcaacgagccagaggttctatatttgcgtctgataagatcttgcacctgtg	60
Db	1	ATGATTTCACAGGGCCAGGTTCTTATGTATAGTACGTGCTATAGGATATGGAACTGTGGG	60
QY	61	gacacttgctcgtacacagctctccagattcccttgctgtlaagctbaagagagggccact	120
Db	61	GACATTGTGATGTACACAGTCTCCATCCCTCCCTACCTGTGTACAGTTGGAGAAAGGTTACT	120
QY	121	attagctggcaaatccagtcagtcagctctgcctcaacagcttgaaccggaggaactacttgct	180
Db	121	ATGAGCTCCAGATCCAGTCACAGGCGCTTTTACTAGCTGTGTACAGTTGGAGAAAGGTTACT	180
QY	181	tggtaccagacgaagaacagagcgacccctccaaactctgtactctactggtgcatccactagg	240
Db	181	TGGTACACAGCAGAAACCAAGGCACTTCCTTAACCTGCTGATTTTACTGGCATCTACTAGG	240
QY	241	gaactctgggtgctcccttgatcgtcttcaagtgtgacgttggaaacgaattcaactctcacc	300
Db	241	GAATCTGGGGTTCCTGTATCCGCTTCACAGGCAAGTGTGAGATCTGGGAACAGATTTCACCTCACC	300
QY	301	atcagcagctctgcagagctgaagaacgtgtgacgtttattactgtcacgcgaactctata--at	357
Db	301	ATCAGCAGTGTGAAGCGCTGAAGACCTGGCAGTTTATCTGTACAGCAATATTATAGCTAT	360
QY	358	cttcaacgcttcgcagacaggaggaaccaagtgtaataataa	396
Db	361	CCATTCAAGTTTCGGCTCGGGGACCAAAAGTTGGAATAATAAA	399

RESULT 4
 US-08-403-853-15
 : Sequence 15, Application US/08403853
 : Patent No. 5844094
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: HUDSON, Peter J.
 : APPLICANT: LAH, Maria
 : APPLICANT: KORRT, Alex A.
 : APPLICANT: IRVING, Robert A.
 : APPLICANT: ATWELL, John L.
 : APPLICANT: MAURY, Rodyn L.
 : APPLICANT: POWER, Barbara E.
 : APPLICANT: COLMAN, Peter M.
 : TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
 :
 : NUMBER OF SEQUENCES: 25
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : CITY: Washington
 :
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20007-5109
 :
 : COMPUTER READABLE FORM:
 :
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/403,853
 : FILING DATE: 30-MAY-1995
 : CLASSIFICATION: 435
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: WO PCT/AU93/00491
 : FILING DATE: 24-SEP-1993
 :
 : PRIOR APPLICATION DATA:

```

1  APPLICATION NUMBER: AU PL 4973
2
3  FILING DATE: 25-SEP-1992
4
5  ATTORNEY/AGENT INFORMATION:
6
7  NAME: BENT, Stephen A.
8
9  REGISTRATION NUMBER: 29,768
10
11 REFERENCE/DOCKET NUMBER: 16786/189/CHAC
12
13 TELECOMMUNICATION INFORMATION:
14
15 TELEPHONE: (202)672-5300
16
17 TELEFAX: (202)672-5399
18
19 TELEX: 904136
20
21 INFORMATION FOR SEQ ID NO: 15:
22
23 SEQUENCE CHARACTERISTICS:
24
25 LENGTH: 870 base pairs
26
27 TYPE: nucleic acid
28
29 STRANDEDNESS: single
30
31 TOPOLOGY: linear
32
33 FEATURE:
34
35 NAME/KEY: mat_peptide
36
37 LOCATION: 40..834
38
39 FEATURE:
40
41 NAME/KEY: CDS
42
43 LOCATION: 40..834
44
45 US-08-0403-853-15

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Query Match	69.6%;	Score 275.8;	DB 3;	Length 870;
Best Local Similarity	89.0%;	Pred. No. 1.2e-79;		
Matches 298;	Conservative	0;	Mismatches 37;	Indels 0;

QY	61	gaactctgctgcagacaagctccacagattccctgctgctgtaagctlaagaaagagagccact	120
Db	463	GACATCGCATGTCACAGTCTCCATCCCTCCCTGGCTGTGTCACTAGGAGAGAGGTCACT	522
QY	121	attgctctgcaaatccagtcagagtcctgctcacaagctagaaccgagaggaactacttgctc	180
Db	523	ATGAGCTGCACAAATCCACTCAGCTCAGCTCTTTCAACAGTGTGAACCCGAAAGAACTACTTGACT	582
QY	181	tgtgtaaccagacgaacacagagcagctccctccaaactgtgtgtatctactctggtatccactagg	240
Db	583	TGTGTACCAAGCAAGAAACCAAGGGCATCTCTCTAAACCGCTGATCTACTGTGGCATCCACTAGG	642
QY	241	gaatctgggggtcccttgatctgctcttaagtgtgcagtgatctctggacaagatttcaactcacc	300
Db	643	GAATCTGGGGTCCCTTGATCGCTTTCACAGGAGTGGATCTGGGACAGATTTCACTCTCACCC	702
QY	301	atccagcagctctgcagagctctgaagacgtgtgcagtttatattactctgcacgcaatctlaaatctt	360
Db	703	ATCAGCAGCTGTGCAGGCGCTGAAGACCTTGCGAGATTTATTTACTGCAAGCAATCTTAAATCTT	762
QY	361	tacacgcttcggacagagggaccaggtggaataaa	395
Db	763	CGGAGCTTCGGGTGGAGGACCAACTCTGGAATTTAA	797

RESULT 5
 US-07-916-098A-54
 : Sequence 54, Application US/07916098A
 : Patent No. 5871732
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: BURKLY, LINDA C.
 : APPLICANT: CHISHOLM, PATRICIA L.
 : APPLICANT: THOMAS, DAVID W.
 : APPLICANT: ROSA, MARGARET D.
 : APPLICANT: ROSA, JOSEPH J.
 :
 : TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 : TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 : NUMBER OF SEQUENCES: 61
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 : STREET: 10 SOUTH WACKER DRIVE
 : CITY: CHICAGO
 :
 : STATE: ILLINOIS
 :
 : COUNTRY: U.S.A.
 :

Query Match	Similarity	67.5%	Score 267.2	DB 3	Length 1701
Best Local Similarity	81.0%	Pred. 8.9e-77			
Matches 311	Conservative	0	Mismatches 73	Indels	Gaps
QY	13	gccacagttctatatactgctgctgctatggtatctgycaccctgtgggacattgctg	72		
Db	53	gctcaggtctctggggctcctgctgctggtggtggtccaggtgccaagagttatgtgaaag	112		
QY	73	acacagttctccagattccctgtgctgttaagcttagagagagggccacattgctgcaaa	132		
Db	113	accctggtctccagatcccttacctgtgctgctacattggagaggggctactttaaactgcaag	172		
QY	133	tccacgtcagatgctgtctcaacagttgagaaacggaggaanaactgtgctgtgtgacagag	192		
Db	173	tccagttgggagaccttattatattatgtatcccaatcaaaaagaaactattgtgctgtgtaaccag	232		
QY	193	aaacacagggcagcctctctaaactgtgactgtactgtggtcattccactaggaatctgggtc	252		
Db	233	aaaccagggcagccctccctaaactgtgactgtggttactgtggtggtcattccactaggaatctgggtc	292		
QY	253	cctgtatgcttcaatgtgccaatgtgacatgtggtgagacagattcaactccaacatcagcagctt	312		
Db	293	cctgtatgcttcaatgtgccaatgtgacatgtggtgagacagattcaactccaacatcagcagctt	352		
QY	313	caggttgaagacgtggtgaggtttattactgtcagcaagcaatctataactttaaactgttcgga	372		
Db	353	caggttgaagacgtggtgaggtttattactgtcagcaagcaatctataactttaaactgttcgga	412		
QY	373	caggtgacacaaagtgtgaataaaa	396		
Db	413	cgagggaccacaaactgtgacatcaa	436		

```

RESULT 6
US-07-916-098A-55
: Sequence 55, Application US/07916098A
: Patent No. 5871732
: GENERAL INFORMATION:
: APPLICANT: BURKLY, LINDA C.
: APPLICANT: CHISHOLM, PATRICIA L.
: APPLICANT: THOMAS, DAVID W.
: APPLICANT: ROSA, MARGARET D.
: APPLICANT: ROSA, JOSEPH J.
: TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
: NUMBER OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
: STREET: 10 SOUTH WACKER DRIVE
: CITY: CHICAGO
: STATE: ILLINOIS
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORD PERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/916,098A
: FILING DATE: July 24, 1992
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/08843
: FILING DATE: No. 5871732ember 27, 1991
: CLASSIFICATION: 424
: APPLICATION NUMBER: 07/618,542
: FILING DATE: No. 5871732ember 27, 1990
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: JOHN J. MC DONNELL
: REGISTRATION NUMBER: 26,949
: REFERENCE/DOCKET NUMBER: 92,310-G
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 715-1000
: TELEFAX: (312) 715-1234
: TELEX: 910/221-5317
: INFORMATION FOR SEQ ID NO: 55:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1701 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 35..100
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: join(101..437, 782..1101)
: FEATURE:
: NAME/KEY: intron
: LOCATION: 438..781
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1
: OTHER INFORMATION: /note="pMDR1007 insert: pre-5A8
: OTHER INFORMATION: humanized light chain"
: NAME/KEY: exon
: LOCATION: 35..436
: FEATURE:
: NAME/KEY: exon

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FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..399
PCT-US93-11612-1

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Best Local Similarity 80.7%; Pred. No. 3.5e-76;
Matches 322; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 1 atgattcacagagccaggtcttattatgtctgtatggtatcgtgacactgtggtg 60
DB 1 atgattcacagagccaggtcttattatgtctgtatggtatcgtgacactgtggtg 60
QY 61 gacattgtctgacacagcttcacagatccctgtgctgtaagcttaagagagagccact 120
DB 61 gacattgtctgacacagcttcacagatccctgtgctgtaagcttaagagagagccact 120
QY 121 atgactgcaaaatccagctcagatctgtcacaacgttagaacccgagagactcttgct 180
DB 121 atgactgcaaaatccagctcagatctgtcacaacgttagaacccgagagactcttgct 180
QY 181 tggtagcagagagaacacagagcagctccctaaactgctgtatcactgagcaccactag 240
DB 181 tggtagcagagagaacacagagcagctccctaaactgctgtatcactgagcaccactag 240
QY 241 gaacttgggtccctgtacgtcttcagtgagtgagatcgtgagacagattcactcacc 300
DB 241 gaacttgggtccctgtacgtcttcagtgagtgagatcgtgagacagattcactcacc 300
QY 301 atcagcagtgctgacagcttgagacagcttgagacagcttgagacagcttgagacag 360
DB 301 atcagcagtgctgacagcttgagacagcttgagacagcttgagacagcttgagacag 360
QY 358 cttaacagcttcgagacagagagagagagagagagagagagagagagagagagag 396
DB 361 ccgctcacgttccgtgctgctggagacacagcttgagagagagagagagagagag 399

RESULT 9
US-07-916-098A-34
Sequence 34, Application US/07916098A
Patient No. 5871732

GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916, 098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/518, 542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1
OTHER INFORMATION: /note= "PMDR1003 insert"

Query Match 62.7%; Score 248.2; DB 3; Length 344;
Best Local Similarity 84.1%; Pred. No. 6.2e-71;
Matches 280; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 60 ggaacattgtgctgacacacatctccagatccctgtgctgtaagcttaagagagagagccac 119
DB 10 ggaacattgtgctgacacacatctccagatccctgtgctgtaagcttaagagagagagccac 119
QY 120 tattagctgaatccagctcagatctgtcacaacgttagaacccgagagagagagagagag 179
DB 70 tattagctgaatccagctcagatctgtcacaacgttagaacccgagagagagagagagag 179
QY 180 ttggtaccagagaaacacag 239
DB 130 ctggtacacagacagaaacacagagagagagagagagagagagagagagagagagagag 239
QY 240 ggaattgggtccctgtacgtcttcagtgagtgagatcgtgagacagattcactcacc 299
DB 190 ggaattgggtccctgtacgtcttcagtgagtgagatcgtgagacagattcactcacc 299
QY 300 catcagcagcttcgagcag 359
DB 250 catcagcagcttcgagcag 359
QY 360 ttacacgcttcgagcag 392
DB 310 tcgacagcttcgagcag 392

RESULT 10
US-08-467-420A-50
Sequence 50, Application US/08467420A


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? Patent No. 5683892
? GENERAL INFORMATION:
? APPLICANT: Ames, Robert S.
? APPLICANT: Appelbaum, Edward R.
? APPLICANT: Chaiken, Irwin M.
? APPLICANT: Cook, Richard M.
? APPLICANT: Gross, Mitchell S.
? APPLICANT: Holmes, Stephen D.
? APPLICANT: McMillan, Lynette J.
? APPLICANT: Theisen, Timothy W.
? TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
? TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
? NUMBER OF SEQUENCES: 74
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: SmithKline Beecham Corp./Corporate
? ADDRESSEE: Intellectual Property
? STREET: P. O. Box 1539-UW2220
? CITY: King of Prussia
? STATE: Pennsylvania
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,420A
? FILING DATE:
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/363131
? FILING DATE: 23-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Sutton, Jeffrey A.
? REGISTRATION NUMBER: 34,028
? REFERENCE/DOCKET NUMBER: P50282
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610 270-5024
? TELEFAX: 610 270-5090
? INFORMATION FOR SEQ ID NO: 50:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5703 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? US-08-467-420A-50

Query Match 62.4%; Score 247; DB 1; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

OY 1 atgattcacagagccaggtcttataatgtctgctcatgtgagatccgtgagg 60
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DB 1014 ATGGTGTTCAGACACCGAGCTTTCATTTCTGTGCTCGATCTCGGCGCTACGGG 1073

OY 61 gacattgtctgacacagctctcagatccctggtctgttaagcttaagagagggccact 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1074 GATATCGTAGAGCCAGCTCCAGACTCGCTAGCTGTCTCGGGGAGAGGGCCACCC 1133

OY 121 attagctgcgaatcagtcagtcagtcctcaacagtagaacccgagagaaactactgtgct 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1134 ATCAACTGCAAGAGCTCTCAAGTCTGTTAAACAGTGAATCAAAAGAACTACTTGCC 1193

OY 181 tggtaaccagagaacacagcagcctcctcaactgctgactactggtgcatccactagg 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1194 TGGATATAGCAGAAACCCGGGACACCTCTAAGTTGCTCATTTACGGGGGCTCAGACTAGG 1253

OY 241 gaactcgtgggtccctgactcgtctcagtgagcagtgatctggagacagattcaacttcacc 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1254 GAATCTGGGCTACTGACCCGATTCAGTGGCAGCGGGTCTGGAGACGATTTCACCTCACC 1313
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OY 301 atcagcaagctgcagagcctgaagcgtgagcagttattactcagcgaactcttaatactt 360
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DB 1314 ATCAGCAGCCTGCAAGGCTGAAGAGATGTGGCAGTATACCTGTGCAGAAATTCATAGTTT 1373

OY 361 --tacacgttcgagcagagggagaccaaggtggaataaa 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1374 CCATTCACGCTCGGGGAGGAGGACCAAGTTGAGATCAAA 1412

RESULT 11
US-08-470-110A-50
? Sequence 50, Application US/08470110A
? Patent No. 5693323
? GENERAL INFORMATION:
? APPLICANT: Ames, Robert S.
? APPLICANT: Appelbaum, Edward R.
? APPLICANT: Chaiken, Irwin M.
? APPLICANT: Cook, Richard M.
? APPLICANT: Gross, Mitchell S.
? APPLICANT: Holmes, Stephen D.
? APPLICANT: McMillan, Lynette J.
? APPLICANT: Theisen, Timothy W.
? TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
? TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
? NUMBER OF SEQUENCES: 74
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: SmithKline Beecham Corp./Corporate
? ADDRESSEE: Intellectual Property
? STREET: P. O. Box 1539-UW2220
? CITY: King of Prussia
? STATE: Pennsylvania
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/470,110A
? FILING DATE:
? CLASSIFICATION: 426
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/363131
? FILING DATE: 23-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Sutton, Jeffrey A.
? REGISTRATION NUMBER: 34,028
? REFERENCE/DOCKET NUMBER: P50282
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610 270-5024
? TELEFAX: 610 270-5090
? INFORMATION FOR SEQ ID NO: 50:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5703 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? US-08-470-110A-50

Query Match 62.4%; Score 247; DB 2; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4.5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

OY 1 atgattcacagagccaggtcttataatgtctgctcatgtgagatccgtgagg 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1014 ATGGTGTTCAGACACCGAGCTTTCATTTCTGTGCTCGATCTCGGCGCTACGGG 1073

OY 61 gacattgtctgacacagctctcagatccctggtctgttaagcttaagagagggccact 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 1074 GATATCGTATGATGACCCAGCTCTCCAGACTGCTAGCTGTGTCTGTGGGAGAGGCCACC 1133
Qy 121 attagctgaataatccagctagctgtctgtccacagtagaacccgagagactacttgct 180
Db 1134 ATCAACTGCAAGAGCTCTAGAGTCTGTTAAACAGGAAATCAAAAGAACTACTTGCC 1193
Qy 181 tggtaacagcagaacacagcagcctccctaactgctgctactgctgacccactag 240
Db 1194 TGGTATCAGACAAACCCGGGAGAGCTCTAGTGTCTGCTATTAGCGGCGTCACTAG 1253
Qy 241 gaactggtggtccctgactgctcagctgagctgagctgagctgagcagattcactacc 300
Db 1254 GAATCTGGGGTCTGACCGATTGAGTGGCAGCGGGTCTGGAGAGATTCTACTCACC 1313
Qy 301 atcagcagctcagcagctgagcagctgagctgagctgagctgagcagcagcttactct 360
Db 1314 ATCAGACGCTCAGGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1373
Qy 361 ---tacagcttcgacagaggggacacaggtggaataaaa 396
Db 1374 CCATTCACGCTCGGGGAGGAGCAAGTGGAGATCAAA 1412

RESULT 12
US-08-667-769A-50
; Sequence 50, Application US/08667769A
; Patent No. 5783184

GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,769A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024

TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-667-769A-50

Query Match 62.4%; Score 247; Length 5703;
Best Local Similarity 77.9%; Pred. No. 4,5e-70;
Matches 311; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

Qy 1 atggaattacagagcccaagcttctatattgctgtcgtcattggtatctgcaactgtg 60
Db 1014 ATGGTGTGACAGACCCAGAGCTTCAATTCCTGTTGCTGTGATCTGATCTGATCTG 1073
Qy 61 gacattggtgacagcagctccagattccctggtggtgagcttgaagagagagccact 120
Db 1074 GATATCGTATGATGACCCAGTCTCCAGACTCGCTAGTGTGTCTGTGGGAGAGGCCACC 1133
Qy 121 attagctgaataatccagctagctgtctcaacagtagaacccgagagactacttgct 180
Db 1134 ATCAACTGCAAGAGCTCTAGAGTCTGTTAAACAGTGAATCAAAAGAACTACTTGCC 1193
Qy 181 tggtaacagcagaacacagcagcctccctaactgctgctactgctgacccactag 240
Db 1194 TGGTATCAGACAAACCCGGGAGAGCTCTAGTGTCTGCTATTAGCGGCGTCACTAG 1253
Qy 241 gaactggtggtccctgactgctcagctgagctgagctgagcagattcactacc 300
Db 1254 GAATCTGGGGTCTGACCGATTGAGTGGCAGCGGGTCTGGAGAGATTCTACTCACC 1313
Qy 301 atcagcagctcagcagctgagcagctgagctgagctgagctgagcagcagcttactct 360
Db 1314 ATCAGACGCTCAGGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1373
Qy 361 ---tacagcttcgacagaggggacacaggtggaataaaa 396
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RESULT 13
US-08-940-371-50
; Sequence 50, Application US/08940371
; Patent No. 5851525

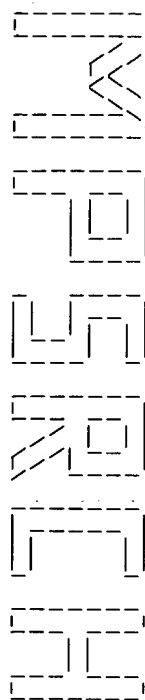
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

Sun Aug 27 09:11:16 2000

us-09-249-011-7.rni

Page 11



(TW)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch.pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Aug 7 19:03:11 2000; Maspar time 12.30 Seconds
Tabular output not generated. 506.103 Million cell updates/sec

Title: >US-09-249-011-8
Description: (1-132) from US09249011.pap
Perfect score: 943
Sequence: 1 MDSQAVLLILLWVSGTGG.....YCGSYNLTFFGGTKEIK 132

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r64
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 41.834; Variance 96.432; scale 0.434

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
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2	777	82.4	120	2	G33932	2.48e-113
3	776	82.3	134	2	S49531	3.74e-113
4	764	81.0	134	1	K4H017	5.23e-111
5	759	80.5	133	1	K4H017	4.09e-110
6	745	79.0	134	2	S21917	1.29e-107
7	744	78.9	138	2	A53261	1.95e-107
8	743	78.8	132	2	PL0014	1.95e-107
9	743	78.8	132	2	S46373	2.94e-107
10	743	78.8	134	2	PC1214	2.94e-107
11	740	78.5	129	2	S40347	1.01e-106
12	734	77.8	240	2	S06084	1.18e-105
13	725	76.9	135	2	S38807	4.76e-104
14	715	75.8	121	1	K4HU	2.87e-102
15	713	75.6	138	2	S26040	6.52e-102
16	709	75.2	124	2	S40364	3.36e-101
17	700	74.2	136	2	A49137	1.34e-99
18	694	73.6	113	2	PR0407	1.56e-98
19	688	73.0	120	2	S51147	1.82e-97
20	683	72.4	114	1	K4H017	1.40e-96
21	682	72.3	112	1	S43103	2.11e-96
22	680	72.1	129	2	S40329	4.79e-96
23	679	72.0	113	2	S34002	7.20e-96

24	675	71.6	113	2	PR0408	Ig light chain V regi	3.69e-95
25 <td>669<td>70.9<th>112</th><th>2</th><th>PL0265</th><th>Ig kappa chain V regi</th><th>4.28e-94</th></td></td>	669 <td>70.9<th>112</th><th>2</th><th>PL0265</th><th>Ig kappa chain V regi</th><th>4.28e-94</th></td>	70.9 <th>112</th> <th>2</th> <th>PL0265</th> <th>Ig kappa chain V regi</th> <th>4.28e-94</th>	112	2	PL0265	Ig kappa chain V regi	4.28e-94
26 <td>666<th>70.6</th><th>113</th><th>2</th><th>S30520</th><th>Ig kappa chain V regi</th><th>1.46e-93</th></td>	666 <th>70.6</th> <th>113</th> <th>2</th> <th>S30520</th> <th>Ig kappa chain V regi</th> <th>1.46e-93</th>	70.6	113	2	S30520	Ig kappa chain V regi	1.46e-93
27 <td>657<th>69.7</th><th>103</th><th>2</th><th>PH1047</th><th>Ig light chain V regi</th><th>5.73e-92</th></td>	657 <th>69.7</th> <th>103</th> <th>2</th> <th>PH1047</th> <th>Ig light chain V regi</th> <th>5.73e-92</th>	69.7	103	2	PH1047	Ig light chain V regi	5.73e-92
28 <td>655<th>69.5</th><th>112</th><th>2</th><th>S41393</th><th>Ig kappa chain V regi</th><th>1.29e-91</th></td>	655 <th>69.5</th> <th>112</th> <th>2</th> <th>S41393</th> <th>Ig kappa chain V regi</th> <th>1.29e-91</th>	69.5	112	2	S41393	Ig kappa chain V regi	1.29e-91
29 <td>650<th>68.9</th><th>103</th><th>2</th><th>PH1052</th><th>Ig light chain V regi</th><th>9.94e-91</th></td>	650 <th>68.9</th> <th>103</th> <th>2</th> <th>PH1052</th> <th>Ig light chain V regi</th> <th>9.94e-91</th>	68.9	103	2	PH1052	Ig light chain V regi	9.94e-91
30 <td>647<th>68.6</th><th>114</th><th>2</th><th>S44119</th><th>Ig kappa chain V regi</th><th>3.37e-90</th></td>	647 <th>68.6</th> <th>114</th> <th>2</th> <th>S44119</th> <th>Ig kappa chain V regi</th> <th>3.37e-90</th>	68.6	114	2	S44119	Ig kappa chain V regi	3.37e-90
31 <td>642<th>68.1</th><th>111</th><th>2</th><th>S03304</th><th>Ig kappa chain V regi</th><th>2.59e-89</th></td>	642 <th>68.1</th> <th>111</th> <th>2</th> <th>S03304</th> <th>Ig kappa chain V regi</th> <th>2.59e-89</th>	68.1	111	2	S03304	Ig kappa chain V regi	2.59e-89
32 <td>642<th>68.1</th><th>113</th><th>2</th><th>S34003</th><th>Ig kappa chain V regi</th><th>2.59e-89</th></td>	642 <th>68.1</th> <th>113</th> <th>2</th> <th>S34003</th> <th>Ig kappa chain V regi</th> <th>2.59e-89</th>	68.1	113	2	S34003	Ig kappa chain V regi	2.59e-89
33 <td>642<th>68.1</th><th>114</th><th>2</th><th>S44116</th><th>Ig kappa chain V regi</th><th>2.59e-89</th></td>	642 <th>68.1</th> <th>114</th> <th>2</th> <th>S44116</th> <th>Ig kappa chain V regi</th> <th>2.59e-89</th>	68.1	114	2	S44116	Ig kappa chain V regi	2.59e-89
34 <td>641<th>68.0</th><th>104</th><th>2</th><th>PH1102</th><th>Ig light chain V regi</th><th>8.77e-89</th></td>	641 <th>68.0</th> <th>104</th> <th>2</th> <th>PH1102</th> <th>Ig light chain V regi</th> <th>8.77e-89</th>	68.0	104	2	PH1102	Ig light chain V regi	8.77e-89
35 <td>639<th>67.8</th><th>104</th><th>2</th><th>PH1102</th><th>Ig light chain V regi</th><th>8.77e-89</th></td>	639 <th>67.8</th> <th>104</th> <th>2</th> <th>PH1102</th> <th>Ig light chain V regi</th> <th>8.77e-89</th>	67.8	104	2	PH1102	Ig light chain V regi	8.77e-89
36 <td>638<th>67.7</th><th>104</th><th>2</th><th>PH1104</th><th>Ig light chain V regi</th><th>1.32e-88</th></td>	638 <th>67.7</th> <th>104</th> <th>2</th> <th>PH1104</th> <th>Ig light chain V regi</th> <th>1.32e-88</th>	67.7	104	2	PH1104	Ig light chain V regi	1.32e-88
37 <td>637<th>67.6</th><th>103</th><th>2</th><th>PH1051</th><th>Ig light chain V regi</th><th>1.98e-88</th></td>	637 <th>67.6</th> <th>103</th> <th>2</th> <th>PH1051</th> <th>Ig light chain V regi</th> <th>1.98e-88</th>	67.6	103	2	PH1051	Ig light chain V regi	1.98e-88
38 <td>633<th>67.1</th><th>101</th><th>2</th><th>PH1046</th><th>Ig light chain V regi</th><th>1.01e-87</th></td>	633 <th>67.1</th> <th>101</th> <th>2</th> <th>PH1046</th> <th>Ig light chain V regi</th> <th>1.01e-87</th>	67.1	101	2	PH1046	Ig light chain V regi	1.01e-87
39 <td>633<th>67.1</th><th>113</th><th>2</th><th>S30523</th><th>Ig kappa chain V regi</th><th>1.01e-87</th></td>	633 <th>67.1</th> <th>113</th> <th>2</th> <th>S30523</th> <th>Ig kappa chain V regi</th> <th>1.01e-87</th>	67.1	113	2	S30523	Ig kappa chain V regi	1.01e-87
40 <td>632<th>67.0</th><th>103</th><th>2</th><th>PH1050</th><th>Ig light chain V regi</th><th>1.51e-87</th></td>	632 <th>67.0</th> <th>103</th> <th>2</th> <th>PH1050</th> <th>Ig light chain V regi</th> <th>1.51e-87</th>	67.0	103	2	PH1050	Ig light chain V regi	1.51e-87
41 <td>632<th>67.0</th><th>131</th><th>2</th><th>S40372</th><th>Ig kappa chain V-J re</th><th>1.51e-87</th></td>	632 <th>67.0</th> <th>131</th> <th>2</th> <th>S40372</th> <th>Ig kappa chain V-J re</th> <th>1.51e-87</th>	67.0	131	2	S40372	Ig kappa chain V-J re	1.51e-87
42 <td>627<th>66.5</th><th>104</th><th>2</th><th>PH1103</th><th>Ig light chain V regi</th><th>1.16e-86</th></td>	627 <th>66.5</th> <th>104</th> <th>2</th> <th>PH1103</th> <th>Ig light chain V regi</th> <th>1.16e-86</th>	66.5	104	2	PH1103	Ig light chain V regi	1.16e-86
43 <td>626<th>66.4</th><th>136</th><th>2</th><th>S40357</th><th>Ig kappa chain V-J re</th><th>1.74e-86</th></td>	626 <th>66.4</th> <th>136</th> <th>2</th> <th>S40357</th> <th>Ig kappa chain V-J re</th> <th>1.74e-86</th>	66.4	136	2	S40357	Ig kappa chain V-J re	1.74e-86
44 <td>623<th>66.1</th><th>113</th><th>2</th><th>PL0263</th><th>Ig kappa chain V regi</th><th>5.88e-86</th></td>	623 <th>66.1</th> <th>113</th> <th>2</th> <th>PL0263</th> <th>Ig kappa chain V regi</th> <th>5.88e-86</th>	66.1	113	2	PL0263	Ig kappa chain V regi	5.88e-86
45 <td>621<th>65.9</th><th>126</th><th>2</th><th>S40339</th><th>Ig kappa chain - huma</th><th>1.33e-85</th></td>	621 <th>65.9</th> <th>126</th> <th>2</th> <th>S40339</th> <th>Ig kappa chain - huma</th> <th>1.33e-85</th>	65.9	126	2	S40339	Ig kappa chain - huma	1.33e-85

ALIGNMENTS

RESULT 1
ENTRY PS0023 #type complete
TITLE Ig kappa chain precursor V region (6A4) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 13-Sep-1998

ACCESSIONS PS0023
REFERENCE PS0023
#authors Margot, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.;
#journal Gene (1988) 74:335-345
#title Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas aeruginosa outer membrane protein I.
#cross-references MIM:89232725
#accession PS0023
##molecule_type mRNA
##residues 1-133 ##label VAR
##experimental_source strain BALB/c
##note the amino-terminal four residues of the mature protein were directly sequenced

COMMENT This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa lipoprotein I.
CLASSIFICATION #superfamily Immunoglobulin V region; Immunoglobulin homology
KEYWORDS heterotetramer; Immunoglobulin
FEATURE 1-20
21-133

SUMMARY #domain signal sequence #status predicted #label SIG
#product Ig kappa chain V region 6A4 #status experimental #label IGV
#length 133 #molecular-weight 14513 #checksum 1662

Query Match 86.9%; Score 819; DB 2; Length 133;
Best Local Similarity 86.4%; Pred. No. 7.45e-121;
Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Db	1	MDSQAVLLILLWVSGTGGTGGVDRFTGSGGDFLTITSSVOAEDLAVYCKOSYNL	60
Qy	1	MDSQAVLLILLWVSGTGGTGGVDRFTGSGGDFLTITSSVOAEDLAVYCKOSYNL	60
Db	61	WYQKPGGPKLLIYMASTRSGVDRSGSGSGTDFLTITSSVOAEDLAVYCKOSYNL	120
Qy	61	WYQKPGGPKLLIYMASTRSGVDRSGSGSGTDFLTITSSVOAEDLAVYCKOSYNL	120
Db	121	RTFGGKTKEIK 132	
Qy	121	RTFGGKTKEIK 132	

```

RESULT      4
ENTRY      4
TITLE      K4H17
ORGANISM   Ig kappa chain precursor V-IV region (B17) - human
DATE       30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
16-Aug-1996

ACCESSIONS
REFERENCE   A01905
#authors   Marsh, P.; Mills, F.; Gould, H.
#journal   Nucleic Acids Res. (1985) 13:6531-6544
#title     Detection of a unique human V kappa avy germline gene by a
           cloned cDNA probe.
#cross-references MIMD:86041854

#accession A01905
#molecule_type mRNA
#residues  1-134 ##label MAR
#note      the sequence was determined from the differentiated gene
#note      the authors translated the codon TGC for residue 76 as
#note      Trp

COMPLEX
An immunoglobulin heterotrimer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily immunoglobulin V region; immunoglobulin homology
heterotrimer; immunoglobulin

CLASSIFICATION
KEYWORDS   #domain signal sequence #status predicted #label SIG\
FEATURE    #product Ig kappa chain V-IV region (B17) #status
           predicted #label MAR\
1-20       #region framework 1\
21-134     #region complementarity-determining 1\
           #region framework 2\
           #region complementarity-determining 2\
           #region framework 3\
           #region complementarity-determining 3\
           #region framework 4\
           #disulfide_bonds #status predicted
SUMMARY    #length 134 #molecular_weight 14863 #checksum 2111

Query Match      81.0%; Score 764; DB 1; Length 134;
Best Local Similarity 84.2%; Pred. No. 5,23e-11;
Matches 112; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

Db 1 MYLDTQVFLSLMISAGVDIMYQSPSLAVSLGERTATCKSSQSLIYSSDNKAYLA 60
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Oy 1 MDSQAQVLLILLMVSQTCGDYLTQSPSLAVSLGERTATCKSSQSLNSTRRENTLA 60

Db 61 WYQQRPGQPKRLIYCASTRESGVPRFGSGSGGDTFTITSLQAEVAVYYCCQYYNL 120
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Oy 61 WYQQRPGQPKRLIYASTRESGVPRFGSGSGGDTFTITSLQAEVAVYYCTQSYNL 120
      ||||| | | | | | | | | | | | | | | | | | | | | | | |

Db 121 PWTFGGCTKVEIK 133
      ||||| | | | | | | | | | | | | | | | | | | | | | | |
Oy 121 -YTFGGCTKVEIK 132

RESULT      5
ENTRY      K4HJ1
TITLE      Ig kappa chain precursor V-IV region (J1) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
22-Jun-1999

ACCESSIONS
REFERENCE   A01904
#authors   Klobbe, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.;
           Pohlenz, H.D.; Zachau, H.G.
#journal   Nucleic Acids Res. (1985) 13:6515-6529
#title     Subgroup IV of human immunoglobulin K light chains is encoded
           by a single germ-line gene.
#cross-references MIMD:86041853

```



```

#accession      A01904
#molecule_type DNA
#residues      1-133 ##label KLO
#cross-references GB:200022; GB:X51570; NID:g33156; PIDN:CAA77317.1;
                        PID:g296654
#note          the sequence was determined from the differentiated gene
GENETICS
#gene          GDB:IGKV
#cross-references GDB:119341; OMIM:146980
#map_position  2p12-2p12
#intons
COMPLEX
An immunoglobulin heterotetramer subunit consists of two
identical light (kappa or lambda) and two identical heavy
(alpha, delta, epsilon, gamma, or mu) chains usually
stabilized by interchain disulfide bonds. In some cases,
such as IgA and IgM, the subunits associate into larger
oligomers.
#superfamily  immunoglobulin V region; immunoglobulin homology
heterotrimer; immunoglobulin
CLASSIFICATION
KEYWORDS
FEATURE
1-20
21-133
21-43
44-60
61-75
76-82
83-114
115-122
123-133
43-114
#length 133 #molecular-weight 14632 #checksum 1869
SUMMARY
Query Match      80.5%; Score 759; DB 1; Length 133;
Best Local Similarity 82.7%; Pred. No. 4,09e-110;
Matches 110; Conservative 8; Mismatches 13; Indels 2; Gaps 2;

Db 1 MWLQVVFSLLMISGANGDIYMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYLA 60
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 1 MDSQAVLLILLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRNYLA 60
      |||||
Db 61 WYQQRPGQPKLLIYVASTRESGVPRFSSGSGTPTLTITSSLOADVAIVYVCOQ-YDT 119
      |||||
QY 61 WYQQRPGQPKLLIYVASTRESGVPRFSSGSGTPTLTITSSLOADVAIVYVCOQSYNL 120
      |||||
Db 120 IPTFGGGRVKEIK 132
      |||||
QY 121 Y-TFGGGRVKEIK 132
      |

RESULT 6
ENTRY      S21917 #type complete
TITLE      Ig kappa chain V region precursor - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change
                        23-Jul-1999
ACCESSIONS S21917
REFERENCE  S21916
#authors   Mierau, R.; Gause, A.; Kneppers, R.; Michels, M.; Magede,
#submission R.A.; Jefferis, R.; Genth, E.
#description submitted to the EMBL Data Library, July 1991
                        A human monoclonal IgA rheumatoid factor using the VK(IV)
                        light chain gene.
#accession  S21917
#status     preliminary
#molecule_type DNA
#residues  1-134 ##label MIE
#cross-references EMBL:X61125; NID:g33288; PIDN:CAA43437.1; PID:g33289
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
                        heterotrimer; immunoglobulin
SUMMARY    #length 134 #molecular-weight 14796 #checksum 3898

Query Match      79.0%; Score 745; DB 2; Length 134;

```

[illegible]

KEYWORDS	immunoglobulin
SUMMARY	#length 135 #molecular-weight 14572 #checksum 4933
Query Match	76.9%; Score 725; DB 2; Length 135;
Best Local Similarity	77.4%; Pred. No. 4,76e-104;
Matches	103; Conservative 16; Mismatches 13; Indels 1; Gaps 1;
Db	3 MESOTOVLISLFWVSGTGGDIYMTSPSSILFVSAKEKYMSKSSQSLFNSGTOKNTLA 62
QY	1 MDSQAGVLLILLMLWVGSTGDIYLTSPDLSLIGERATISCKSSQSLNSRTRENTYA 60
Db	63 WYQKPEQPKLLIYASTRESGVDPFRFGSSGSDFTLTSSVQAEADVAAYYQCNHSY 122
QY	61 WYQKPEQPKLLIYASTRESGVDPFRFGSSGSDFTLTSSVQAEADVAAYYQCTOSYNL 120
Db	123 PYTFGGGTKLIDIN 135
QY	121 -YTFGGGTKEIK 132
RESULT	14
ENTRY	KAHU
TITLE	Ig kappa chain precursor V-IV region - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
ACCESSIONS	A01902
REFERENCE	A93589
#authors	Klobbeck, H.G.; Bornkamm, G.W.; Combariato, G.; Mocikat, R.;
#journal	Pohlentz, H.D.; Zachau, H.G.
#title	Nucleic Acids Res. (1985) 13:6515-6529
#cross-references	Subgroup IV of human immunoglobulin K light chains is encoded by a single germline gene.
#accession	WJID:86041853
#molecule_type	DNA
#residues	1-121 ##label KIO
#note	the sequence was determined from the germline gene
GENETICS	there is only one Ig kappa V-IV gene
#introns	17/1
COMPLEX	An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
CLASSIFICATION	#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; immunoglobulin
KEYWORDS	#domain signal sequence #status predicted #label SIG
FEATURE	#product ig kappa chain precursor V-IV region #status predicted #label MAT
1-20	#region framework 1\
21-121	#domain immunoglobulin homology #label IMM
21-43	#region complementarity-determining 1\
36-116	#region framework 2\
44-60	#region complementarity-determining 2\
61-75	#region framework 3\
76-82	#region complementarity-determining 3\
83-114	#disulfide_bonds #status predicted
115-121	#length 121 #molecular_weight 13380 #checksum 9684
SUMMARY	
Query Match	75.8%; Score 715; DB 1; Length 121;
Best Local Similarity	84.0%; Pred. No. 2,87e-102;
Matches	100; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Db	1 MYLOTQFISLIMIGAGDIYMTSPDLSLIGERATISCKSSQSLNSNNKNTLA 60
QY	1 MDSQAGVLLILLMLWVGSTGDIYLTSPDLSLIGERATISCKSSQSLNSRTRENTYA 60
Db	61 WYQKPEQPKLLIYASTRESGVDPFRFGSSGSDFTLTSSVQAEADVAAYYQCOYYS 119

OY 61 WYQKPGQPKLIYWASTRESGVDPDRFGSGSGTDFTLTISSLAQEDVAVYYCTQSYN 119

RESULT 15

ENTRY S26040 #type fragment

TITLE Ig kappa chain precursor - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 23-Jul-1999

ACCESSIONS S26040: S78098

REFERENCE S09216

#authors Okamoto, M.; Honjo, T.

#journal Nucleic Acids Res. (1990) 18:1895

#title Nucleotide sequences of the gene/cDNA coding for anti-murine erythrocyte autoantibody produced by a hybridoma from NZB mouse.

#cross-references MUID:90245589

#accession S26040

#molecule_type DNA

#residues 1-138 ##label OKA

##cross-references EMBL:X51742

##note the authors translated the codon AGC for residue 107 as Thr and AGT for residue 108 as Thr

REFERENCE S78098

#authors Okamoto, M.

#submission submitted to the EMBL Data Library, February 1990

#accession S78098

#molecule_type DNA

#residues 1-87,'W',89-138 ##label OKW

##cross-references EMBL:X51742; NID:952697; PIDN:CAA36032.1; PID:952698

GENETICS

#introns 22/1

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS heterotetramer; immunoglobulin

FEATURE

1-25 #domain signal sequence #status predicted #label SIG\

26-138 #product Ig kappa chain (fragment) #status predicted

#label MAT

SUMMARY #length 138 #checksum 910

Query Match 75.68; Score 713; DB 2; Length 138;

Best Local Similarity 75.28; Pred. No. 6.52e-102;

Matches 103; Conservative 18; Mismatches 11; Indels 5; Gaps 1;

Db 1 MDSQAOVLMLLLWVSGEKKRSTGCDIVMSGSSSLTVSGEYTMNCKSSQSILYSNNQ 60

OY 1 MDSQAOVLMLLLWVSG-----TCGDIVLTVQSPSLAVSLGERATISCKSSQSILNSRTR 55

Db 61 KNYLAWYQQRPGQPKLIYWASTRESGVDPDRFGSGSGTDFTLTISSVKAEDLAVYFCQ 120

OY 56 ENYLAWYQQRPGQPKLIYWASTRESGVDPDRFGSGSGTDFTLTISSLAQEDVAVYYCT 115

Db 121 QYTSFLTFGAGTKLEK 137

OY 116 QSYNLYTFTGGTKVEIK 132

Search completed: Mon Aug 7 19:03:26 2000

Job time : 15 secs.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 [1]
 RP SEQUENCE.
 RX MEDLINE: 76004342.
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 subgroups IV of the kappa type (Bence-Jones protein Len.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01903; KAHULN.
 DR HSSP: P01789; 2MCP.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 40
 FT DOMAIN 41 55
 FT DOMAIN 56 62
 FT DOMAIN 63 94
 FT DOMAIN 95 101
 FT DOMAIN 102 113
 FT DISULFID 23 94
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
 Query Match 72.7%; Score 686; DB 1; Length 114;
 Best Local Similarity 86.7%; Pred. No. 5,04e-144;
 Matches 98; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
 Db 1 DIWTFSPDCLAVSLGERATICKSSOSVLYSSSKNTLANTYQKPGCPKLLIYMASTR 60
 21 DIVTOSPDLSLAVSLGERATICKSSOSLNSRTRENTLAVYQKPGCPKLLIYMASTR 80
 QY 61 ESVGDPDFSGSGSTDTLTITSSLAQEDVANYQOQYSTRYSRGGCKLEIK 113
 81 ESVGDPDFSGSGSTDTLTITSSLAQEDVANYQOQYSTRYSRGGCKLEIK 132
 RESULT 5
 ID KY2E HUMAN STANDARD; PRT; 133 AA.
 AC P06310;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA Klobbeck H.G., Meindl A., Combario G., Solomon A., Zachau H.G.;
 RT "Human Immunoglobulin kappa light chain genes of subgroups II and
 III".
 RL Nucleic Acids Res. 13:6499-6513(1985).
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 or send an email to license@isb-sib.ch).
 CC EMBL: Z00020; CA77315.1; -.
 DR PIR: A01890; K2HURP.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 133
 FT DOMAIN 21 43
 FT DOMAIN 44 59
 FT DOMAIN 60 74
 FT DOMAIN 75 81
 FT DOMAIN 82 113
 FT DOMAIN 114 122
 FT DOMAIN 123 132
 FT DISULFID 43 113
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;
 Query Match 64.9%; Score 612; DB 1; Length 133;
 Best Local Similarity 64.7%; Pred. No. 8,49e-125;
 Matches 86; Conservative 23; Mismatches 22; Indels 2; Gaps 2;
 Db 1 MRPLPAQLGLMTWPPSSGDVYWTQSPSLPYTLGAPASISCRSSQSLVSDG-NTYLN 59
 1 MDSQAQVLLILLMLVWSTCGDIVLTQSPDSLAVSLGERATICKSSOSLNSRTRENTYLA 60
 QY 60 WFOQRPGQSRRLLYKYSNDSGYDPDFSGSGSTDTLTLSRYEADVGYIYMGOSTH 119
 61 WYQKPGQPKLLIYMASTRBEGVDPDFSGSGSTDTLTITSSLAQEDVANYCTOSYNL 120
 Db 120 SMFPGGCKVEIK 132
 QY 121 -YTFGGCKVEIK 132
 RESULT 6
 ID KY3F MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION MOPC 321 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE OF 1-37.
 RX MEDLINE: 78235887.
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 the variable and constant regions of immunoglobulin light chain
 precursors: implications on the organization and controlled
 expression of immunoglobulin genes.";
 RT Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE: 73140224.
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse Immunoglobulin chains. Partial amino acid sequence of a kappa
 chain.";
 RL Biochemistry 12:749-759(1973).
 CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
 BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
 REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
 RESIDUES.
 DR PIR: A01933; KYMS32.
 DR PRAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 132
 FT DOMAIN 21 43
 FT DOMAIN 44 58
 FT DOMAIN 59 73
 FT DOMAIN 74 80
 FT DOMAIN 81 112
 FT DOMAIN 113 121
 FT DOMAIN 122 131
 FT DISULFID 43 112
 IG KAPPA CHAIN V-III REGION MOPC 321.
 FRAMEWORK 1.
 COMPLEMENTARITY-DETERMINING 1.
 FRAMEWORK 2.
 COMPLEMENTARITY-DETERMINING 2.
 FRAMEWORK 3.
 COMPLEMENTARITY-DETERMINING 3.
 FRAMEWORK 4.
 BY SIMILARITY.

FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BA773FBE9 CRC64;

Query Match 64.2%; Score 605; DB 1; Length 132;
Best Local Similarity 59.4%; Pred. No. 5,49e-123;

Matches 79; Conservative 33; Mismatches 18; Indels 3; Gaps 3;

DB 1 METDPLLLVLLWLPSTGDIYLTQSPASLAVSLQARATISCRASKV-NTYG-NSFMZ 58
1 MSQAQVLLILLMLWSGCGDIVLTQSPDLAVSLGERATISCKSSQSLNSTRNTYLA 60
QY 59 WYZAKRGZPKLLIYRASLZSGIPARFSGSGSRBFTITIBPVZABDVATTFCLZSEB 118
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLAQEDVAVYYCTQSY- 119
DB 119 PWTFGGTVEIK 131
QY 120 LYTFGGGTVEIK 132

RESULT 7
ID KV3M_HUMAN STANDARD; PRT; 129 AA.

AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; P10022; K3H0HA.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B874D6 CRC64;

Query Match 63.5%; Score 599; DB 1; Length 129;
Best Local Similarity 66.2%; Pred. No. 1.95e-121;

Matches 88; Conservative 25; Mismatches 14; Indels 6; Gaps 4;

DB 1 METPALLFLILLMLPDTGTGEIVLTQSPGTLSPGERATLSCRASQSV--S-S--SYLA 55
1 MSQAQVLLILLMLWSGCGDIVLTQSPDLAVSLGERATISCKSSQSLNSTRNTYLA 60
QY 1 WYQKRGQPKLLIYRASLZSGIPARFSGSGSRBFTITIBPVZABDVATTFCLZSEB 118
59 WYZAKRGZPKLLIYRASLZSGIPARFSGSGSRBFTITIBPVZABDVATTFCLZSEB 118
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLAQEDVAVYYCTQSY- 119
DB 116 PWTFGGTVEIK 128
QY 120 LYTFGGGTVEIK 132

RESULT 8
ID KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 88171307.
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RT J. Exp. Med. 167:840-852(1988).
RL -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR; P10022; K3H0HA.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 20
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C552927274D0 CRC64;

Query Match 63.4%; Score 598; DB 1; Length 129;
Best Local Similarity 66.9%; Pred. No. 3.54e-121;
Matches 89; Conservative 25; Mismatches 13; Indels 6; Gaps 4;

DB 1 METPALLFLILLMLPDTGTGEIVLTQSPGTLSPGERATLSCRASQSV--S-S--SYLA 55
1 MSQAQVLLILLMLWSGCGDIVLTQSPDLAVSLGERATISCKSSQSLNSTRNTYLA 60
QY 1 WYQKRGQPKLLIYRASLZSGIPARFSGSGSRBFTITIBPVZABDVATTFCLZSEB 118
59 WYZAKRGZPKLLIYRASLZSGIPARFSGSGSRBFTITIBPVZABDVATTFCLZSEB 118
61 WYQKRGQPKLLIYWASTRESGVDPDRFSGSGSGTDFTLTISLAQEDVAVYYCTQSY- 119
DB 116 PWTFGGTVEIK 128
QY 120 LYTFGGGTVEIK 132

RESULT 9
ID KV3I_MOUSE STANDARD; PRT; 131 AA.

AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE OF 1-35.
RX MEDLINE; 78235887.
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
the variable and constant regions of immunoglobulin light chain

RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes."
 RL Biochemistry 17:2392-2400(1978).
 RN [21
 RP SEQUENCE OF 21-131.
 RX MEDLINE: 73140225.
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences."
 RL Biochemistry 12:760-771(1973).
 RN [3]
 RP REVISIONS.
 RX MEDLINE: 79012520.
 RA McKean D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions."
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR PIR: A01935; KVM5M6.
 DR PIR: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 73 FRAMEWORK 2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 81 112 FRAMEWORK 3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 131 FRAMEWORK 4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
 Query Match 61.9%; Score 584; DB 1; Length 131;
 Best Local Similarity 63.2%; Pred. No. 1,46e-117;
 Matches 84; Conservative 26; Mismatches 20; Indels 3; Gaps 3;
 Db 1 METDILLMVLVWPGSTGNITVLTQSPASLAVSLGQRTATISCRASESY-DSYG-NSFMH 58
 Y 1 MDSQAVILLILLWVSGTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLA 60
 Db 59 WYQKRGPPKLLIYLAWSLNSGVPAFSGSGSRFTDITTPVADDAATYYCOONED 118
 Y 61 WYQKRGPPKLLIYMAWTRRESGVDRFSGSGGTDFLTITSSLAEDVAVYYCQSY-N 119
 Db 119 PWTGGGTKEIK 131
 Y 120 LYTFGGGTKEIK 132
 RESULT 10
 ID KVVH_HUMAN STANDARD: PRT: 129 AA.
 AC P04207;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION CIL PRECURSOR (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86177570.
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Cud J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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 CC
 DR EMBL: M12740; AA58992.1; -.
 DR PIR: A01898; K3HUC1.
 DR HSSP: P01789; 2MCP.
 DR PIR: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3-
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 5613B411BE60CC14 CRC64;
 Query Match 61.7%; Score 582; DB 1; Length 129;
 Best Local Similarity 67.2%; Pred. No. 4.78e-117;
 Matches 90; Conservative 21; Mismatches 15; Indels 8; Gaps 4;
 Db 1 MEAPQLLEFLLMVPDTGETVMTQSPATLSVSGEATISCRASGV--S---NN-LA 54
 Y 1 MDSQAVILLILLWVSGTGCDIVLTQSPDSLAVSLGERATISCKSSQSLNSRRENTLA 60
 Db 55 WYQKRGPPKLLIYAGSTRATGIPARFSGSGGTDFLTITSSRQSEDFAVYYCOQYNNW 114
 Y 61 WYQKRGPPKLLIYMAWTRRESGVDRFSGSGGTDFLTITSSLAEDVAVYYCQSY-N 119
 Db 115 PWTGGGTKEIK 128
 Y 120 LYTFGGGTKEIK 132
 RESULT 11
 ID KVVH_HUMAN STANDARD: PRT: 129 AA.
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85014148.
 RA Klobbeck H.G., Combratio G., Zachau H.G.;
 RT "Immunoglobulin genes of the kappa light chain type from two human
 RT lymphoid cell lines are closely related."
 RL Nucleic Acids Res. 12:6995-7006(1984).
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 CC
 DR EMBL: X00965; CAA25477.1; ALT_TERM.
 DR PIR: A01883; K1HWK.
 DR HSSP: P01607; 1REI.
 DR PIR: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22 IG KAPPA CHAIN V-I REGION WALKER.
 FT CHAIN 23 129
 FT DOMAIN 23 45 FRAMEWORK 1.

FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA: 14069 MW: F941FA07DAFCA2F9 CRC64:

Query Match 58.68; Score 553; DB 1; Length 129;
 Best Local Similarity 65.7%; Pred. No. 1.39e-109;
 Matches 88; Conservative 18; Mismatches 19; Indels 9; Gaps 5;

Db 3 MRYPALLGLLMLMGARC-DIQMTQSPSSLSASVGDRTYICRASQSY--S-----NYL 55
 1 MOSQAOVLILLILMWST-CGDIVLTQSPDSLAVSLGERATICKSSQSLNRTENTYL 59
 Db 56 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 115
 60 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 119
 Db 116 TLTFGQGTREIK 129
 120 -LYTFGQGTREIK 132

RESULT 12
 ID KV3K_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 86041852.
 RA Klobeck H.G., Meindl A., Combrilato G., Solomon A., Zachau H.G.;
 RT Human immunoglobulin kappa light chain genes of subgroups II and
 RT III.
 RL Nucleic Acids Res. 13:6499-6513(1985).
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DR EMBL: Z00021; CAAT7316.1; -;
 DR PIR: A01899; K3H041.
 DR PIR: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 28 IG KAPPA CHAIN V-III REGION IARC/BL41.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 128 JKI SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA: 14070 MW: CC89570FE3B9012 CRC64:

Query Match 58.48; Score 551; DB 1; Length 128;
 Best Local Similarity 64.7%; Pred. No. 4.53e-109;
 Matches 86; Conservative 24; Mismatches 16; Indels 7; Gaps 5;

Db 1 MEHPALLFLLLMLPDTGTGELVLTQSPDTLSLSPESATLSCRASQSY--S-S--N-LA 54
 1 MOSQAOVLILLILMWST-CGDIVLTQSPDSLAVSLGERATICKSSQSLNRTENTYL 60
 Db 55 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 114
 61 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 119
 Db 115 PYTFGQGTREIK 127
 120 -LYTFGQGTREIK 132

RESULT 13
 ID KV3K_HUMAN STANDARD; PRT; 116 AA.

AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION VH PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85087932.
 RA Pech M., Zachau H.G.;
 RT "Immunoglobulin genes of different subgroups are interdigitated
 RT within the VK locus."
 RL Nucleic Acids Res. 12:9229-9236(1984).
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DR EMBL: X02725; -, NOT_ANNOTATED_CDS.
 DR PIR: A01901; K3H0VH.
 DR HSSP: P01789; ZMCP.
 DR PIR: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 1 28 IG KAPPA CHAIN V-III REGION VH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA: 12757 MW: 51CD55BA3B21929 CRC64:

Query Match 56.7%; Score 535; DB 1; Length 116;
 Best Local Similarity 64.2%; Pred. No. 5.76e-105;
 Matches 77; Conservative 24; Mismatches 14; Indels 5; Gaps 3;

Db 1 MEHPALLFLLLMLPDTGTGELVLTQSPDTLSLSPESATLSCRASQSY--S-S--SYLT 55
 1 MOSQAOVLILLILMWST-CGDIVLTQSPDSLAVSLGERATICKSSQSLNRTENTYL 60
 Db 56 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 115
 61 MWYQKPGKAPKLLIYAAASLSQSGVTSRFGSGSGGTDFLTITISLPEDSAFYVCOQSYTS 120

RESULT 14
 ID KV2E_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;

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DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION GM607 PRECUSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 84191506.
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity."
RL Nature 309:73-76(1984).
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CC -----
CC EMBL: Z00009; -; NOT_ANNOTATED_CDS.
DR PIR: A01889; K2HUGM.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK 1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 58 FRAMEWORK 2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 66 97 FRAMEWORK 3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 107 116 FRAMEWORK 4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match
Best Local Similarity 56.7%; Score 535; DB 1; Length 117;
Matches 81; Conservative 13; Mismatches 21; Indels 2; Gaps 2;

Db 1 GSSGDIWVTSPLPYTPGPASISCRSSQSLHSNG-VNYLDWYLOKPOQSPQLIYL 59
Y 17 GTCGDIVLTOSPDLSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPPQPKLLIYW 76

Db 60 GSNRAGVDPDRFSGSGGTDETLKISRVEADGVYVCMOGLQTPQFGQGTKEIK 116
Y 77 ASTRESGVDPDRFSGSGGTDETLTISLQAEADVAVYCTOSYNL-YTFGGGTKEIK 132

RESULT 15
ID KY3P.MOUSE STANDARD; PRT; 110.AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 79073152.
RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
DR PIR: D01937; KVM510.
DR PFAM: PF00047; 1g; 1.

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KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 101 110 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CEB86B1249 CRC64;

Query Match
Best Local Similarity 56.6%; Score 534; DB 1; Length 110;
Matches 79; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

Db 1 DIVTOSPASLAVSLGORATISCKASQSL-DYDG-DSYNNWYQKPPQPKLLIYASNL 58
Y 21 DIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLAWYQKPPQPKLLIYMASTR 80

Db 59 ESGIPARFSGSGGTDETLNHPVEEDATYVCHOSEDPWTGSGTKLEIK 110
Y 81 ESGVDPDRFSGSGGTDETLTISLQAEADVAVYCTOSYNL-YTFGGGTKEIK 132

Search completed: Mon Aug 7 19:02:14 2000
Job time : 9 secs.

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(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

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Run on: Mon Aug 7 19:02:32 2000; MasPar time 17.93 Seconds
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Tabular output not generated.

Sequence: 1 MDSQAQVLILLWVSGTCG.....YCTQSYNLTYFGQGTKEIK 132

Scoring table:

Searched: 225878 seqs, 69334122 residues

Listing first 45 summaries

Database:

13:sp_vertebrate 14:sp_virus

Statistics: Mean 41.466; Variance 66.918; scale 0.620

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	185	19.6	123	11	061243	8HS30 PROTEIN PRECURSO	5.38e-19
2	164	17.4	100	6	077624	SURROGATE LIGHT CHAIN	1.38e-14
3	129	13.7	509	11	008907	BRAIN IMMUNOLOGICAL-L1	1.05e-077
4	124	13.1	513	11	P97797	PROTEIN TYROSINE PHOSP	8.91e-070
5	123	13.0	122	4	Q95604	TRGV9 (FRAGMENT)	1.36e-06
6	123	13.0	122	4	Q95603	TRGV9 (FRAGMENT)	1.36e-06
7	120	12.7	210	6	P79336	CD8 BETA ANTIGEN PRECU	4.80e-066
8	119	12.6	509	11	Q9WTN4	BIT-	7.29e-06
9	118	12.5	81	4	075734	IG HEAVY CHAIN VARIANT	1.10e-05
10	113	12.0	150	4	Q95973	VH4 HEAVY CHAIN VARIANT	8.58e-05
11	113	12.0	198	4	013970	CD8 ANTIGEN-	8.58e-05
12	113	12.0	235	6	Q9XSME	CD8 ALPHA CHAIN PRECUR	8.58e-05
13	111	11.8	169	4	Q9Y2N4	T-CELL RECEPTOR V-GAM	1.92e-04
14	110	11.7	81	4	075736	IG HEAVY CHAIN VARIANT	2.87e-044
15	110	11.7	82	4	075732	IG HEAVY CHAIN VARIANT	2.87e-044
16	107	11.3	77	4	075726	IG HEAVY CHAIN VARIANT	9.45e-044
17	106	11.2	74	4	075744	IG HEAVY CHAIN VARIANT	1.40e-033
18	106	11.2	82	4	075725	IG HEAVY CHAIN VARIANT	1.40e-033
19	106	11.2	150	4	Q91294	IGG VH PROTEIN PRECURS	1.40e-033
20	106	11.2	318	13	091668	CORTICAL THYMOCYTE MAR	1.40e-033

21	105	11.1	81	0.75721	IG HEAVY CHAIN VARIABLE	2.07e-03
22	105	11.1	346	0.60781	DA23G2624.1.	2.07e-03
23	103	10.9	147	0.91509	VH3 PROTEIN (FRAGMENT)	4.50e-03
24	102	10.8	77	0.75741	IG HEAVY CHAIN VARIABLE	6.60e-03
25	102	10.8	167	0.79986	CD8 ALPHA CHAIN (FRAGM	6.60e-03
26	102	10.8	167	0.79985	CD8 ALPHA CHAIN (FRAGM	6.60e-03
27	102	10.8	1142	0.60732	MELANOMA-ASSOCIATED AN	5.00e-03
28	102	10.8	1142	0.75451	CANCER/TESTIS ANTIGEN	6.00e-03
29	99	10.5	78	0.75739	IG HEAVY CHAIN VARIABLE	2.06e-02
30	97	10.3	118	0.92104	ANTI-PORCINE VCAM MAB	4.36e-02
31	97	10.3	200	0.95776	H.NH1021A08.2 PROTEIN.	4.36e-02
32	97	10.3	209	0.95XW7	CD8 BETA CHAIN PRECURS	4.36e-02
33	97	10.3	235	0.90770	CD8 ALPHA CHAIN PRECUR	4.36e-02
34	97	10.3	272	0.70356	BDT1.	4.36e-02
35	97	10.3	288	0.00517	HYDROPHILIN-LIKE (FRA	4.36e-02
36	96	10.2	75	0.75743	IG HEAVY CHAIN VARIABLE	6.32e-02
37	96	10.2	78	0.75723	IG HEAVY CHAIN VARIABLE	6.32e-02
38	96	10.2	259	0.95532	DIJ889W15.1 (NOVEL PROT	6.32e-02
39	96	10.2	506	0.46631	MYD-1 ANTIGEN PRECURSO	6.32e-02
40	96	10.2	4162	0.98918	CONNECTIN/TITIN (FRAGM	6.32e-02
41	96	10.2	5198	0.76518	HENICENTIN PRECURSOR.	6.32e-02
42	94	10.1	86	0.75740	IG HEAVY CHAIN VARIABLE	9.13e-02
43	95	10.1	97	0.43234	RHEUMATOID FACTOR RF-E	9.13e-02
44	95	10.1	401	0.80835	POLIOVIRUS RECEPTOR AL	9.13e-02
45	94	10.0	16	0.79458	LIGHT-CHAIN COMPLEMENTA	1.32e-01

ALIGNMENTS

ID	RESULT
AC	PREDIMINARY; PT; 123 AA.
DT	061243;
PT	01-NOV-1996 (Tremblrel_01, Created)
DT	01-NOV-1998 (Tremblrel_01, Last sequence update)
DT	01-NOV-1999 (Tremblrel_12, Last annotation update)
DE	BHS20 PROTEIN PRECURSOR.
GN	VPREB3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
KP	SEQUENCE FROM N.A.
RC	STRAIN-BALB/C;
RX	MEDLINE; 93259124.
RA	SHIRAAMA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y., RAJESWARY K., TAKEMORI T.; " A novel gene product associated with mu chains in immature B cells."; EMBO J. 12:1827-1834(1993). R.L EMB1; D13208; BA02495.1; -. DR MGD; MG1:98938; Vpreb3. DR PEMAN; PF00047; Ig; 1. FT CHAIN SQ SEQUENCE 123 AA; 13400 MW; DA2AYOD3 CRC32; 8HS20 PROTEIN.
Dc	Query Match 19.6%; Score 185; DB 11; Length 123; Best Local Similarity 36.3%; Pred.No.5.8le-19; Matches 41; Conservative 28; Mismatches 36; Indels 8; Gaps 6;
Oy	7 LPLLIGTFVNVPQPLTLG-PDAFVFEPGDPAHLSC-TINSO-HATAGDIGSVYQQOPG 63 : :: : : : :: Db 8 LIILLMWSGFGDIVLQSFDLSVLASGERATISCKSSQLNSRRRENTLAYQGKPG 67 : DB 64 SAPHLLYYAAEEHYRPADIDPRSAIVDDAHNAHCILTIISVLPEDADDFCS 116 : : : :: : : :: : : : : Oy 68 QPKKLIIYWAST---RESGVPDFRSGGSSGSgt-Df-tLTISSLOAEVDVAAYCYCT 115
RESULT	2
ID	PRELIMINARY; PRT; 100 AA.
AC	077624;
DT	01-NOV-1998 (Tremblrel_08, Created)
DT	01-NOV-1998 (Tremblrel_08, Last sequence update)
DT	01-NOV-1999 (Tremblrel_12, Last annotation update)

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DE SURGATE LIGHT CHAIN (FRAGMENT).
GN VPREB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RA RAYCHEL A.P., HALLIGAN B.D.;
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF068848; AAC19380.1; -.
FT NON_TER 1
FT NON_TER 100
FT NON_TER 100
SQ SEQUENCE 100 AA; 11142 MW; 3785537C CRC32;

Query Match 17.4%; Score 164; DB 6; Length 100;
Best Local Similarity 38.2%; Pred. No. 1,38e-14;
Matches 39; Conservative 19; Mismatches 34; Indels 10; Gaps 9;

Db 3 LLLHRCGCPQVYLSQP-SVASFGLATYRLACTLSSDH-DVNLHSIT--WTQQRPHRP 58
OY 11 LLLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNKRRENTLAWYQKPGQPP 70
DB 59 RFLRYFSPDKRGHKVPPRFSGSKDLAKNTGYLSIAELQA 100
OY 71 K-LLIYMA-S-TRES-GVDPFRFSGSGS-GTDFT-LTISLSQA 106

RESULT 3
ID 008907 PRELIMINARY; PRT: 509 AA.
AC 008907;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE BRAIN IMMUNOLOGICAL-LIKE PROTEIN (BIT).
GN BIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE: 97230468.
RA OHNISHI H., KUBOTA M., SANO S.;
RT "BIT (Bit) maps to mouse chromosome 2.";
RL Genomics 40:504-506(1997).
DR EMBL: D85785; BAA20376.1; -.
DR MGD: MGI:107947; Bit.
DR PFM: PFM0047; Ig: 3.
SQ SEQUENCE 509 AA; 56033 MW; 4C020C08 CRC32;

Query Match 13.7%; Score 129; DB 11; Length 509;
Best Local Similarity 28.4%; Pred. No. 1,05e-07;
Matches 29; Conservative 32; Mismatches 31; Indels 10; Gaps 10;

Db 27 TGATGTEVAVTQPEKSVSAAGDSTILNCTV-SIL-P-V-GP-IMYRG-VGQS-RLII 79
OY 16 SCGCG-DIVLTQSPDSLAVSLGERATISCKSSQSLNKRRENTLAWYQKPGQPPKLLI 74
DB 80 YSTGEHPFRVNVSDTTKRNNMDSFIRISNVTPEDAGTYTC 121
OY 75 Y-WASTRESGVDPFRFSGSG-SGIDFTLTISLQAEVAVTYTC 114

RESULT 4
ID P97797 PRELIMINARY; PRT: 513 AA.
AC P97797; P97796: O35924; O88555; O88556;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR

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DE (P84) (SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SHPS1).
PTPNS1 OR P84 OR SHPS-1 OR SHPS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 97223399.
RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,
RA FUJIOKA Y., KASUGA M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes."
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-53; 422-424 AND 429-433.
RC STRAIN-BALB/C; TISSUE-CEREBELLUM, AND BRAIN;
RX MEDLINE: 98012243.
RA COMU S., MENG W., OLINSKY S., ISHMAD P., MI Z., HEMPEL J., WATKINS S.,
RA LAGENAUER C.F., NARAYANAN V.;
RT "The murine P84 neural adhesion molecule is SHPS-1, a member of the
RT phosphatase-binding protein family."
RL J. Neurosci. 17:8702-8710(1997).
RN [3]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC STRAIN-C57BL/6; TISSUE-FETAL THYMUS;
RX MEDLINE: 98380500.
RA VEILLETTE A., THIBAUDEAU E., LATOUR S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RT with protein tyrosine phosphatase SHP-1 in macrophages."
RL J. Biol. Chem. 273:22719-22728(1998).
RN [4]
RP FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE: 90152134.
RA CHUANG W., LAGENAUER C.F.;
RT "Central nervous system antigen P84 can serve as a substrate for
RT neurite outgrowth."
RL Dev. Biol. 137:219-232(1990).
RN [5]
RP FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
MITOGENS AND CELL ADHESION. PROTEIN SUPPORTS ADHESION OF
CEREBELLAR NEURONS, NEURITE OUTGROWTH AND GLIAL CELL ATTACHMENT.
MAY PLAY A KEY ROLE IN INTRACELLULAR SIGNALING DURING
SYNAPTONEGENESIS AND IN SYNAPTIC FUNCTION. MAY ACT AS A DOCKING
PROTEIN AND INDUCE TRANSLOCATION OF SHP-2 FROM THE CYTOSOL TO THE
PLASMA MEMBRANE; TYROSINE PHOSPHORYLATED PTPNS1 FROM MACROPHAGES
PRIMARILY ASSOCIATES WITH SHP-1.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE FORMS; ISOFORMS 1 (SHOWN HERE), 2 AND
SMALL, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE CEREBRAL CORTEX, CEREBELLUM,
SPINAL CORD, SPLEEN AND MACROPHAGES AND AT MUCH LOWER LEVEL IN THE
KIDNEY, HEART, LIVER AND THYMUS. WITHIN THE CEREBELLUM, EXPRESSION
IS DETECTED IN THE SYNAPTIC GLOMERULI, GRANULE CELL BODIES, GOLGI
EPITHELIAL CELLS, OLFACTORY BULB, NEURONS IN THE HIPPOCAMPUS AND
THE DENTATE GYRUS. IN THE EYE, EXPRESSION IS FIRST SEEN IN THE
INNER PLEXIFORM AND OPTIC FIBER LAYERS, LATER IN DEVELOPMENT
EXPRESSION IS ALSO SEEN IN THE OUTER PLEXIFORM, RETINA AND OUTER
SEGMENTS OF THE PHOTORECEPTOR LAYER.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 7, WHEN
EXPRESSION IS RESTRICTED TO THE FLOOR PLATE REGION OF THE VENTRAL
NEURAXIS. WIDESPREAD EXPRESSION IN A VARIETY OF CNS REGIONS BEGINS
2-5 DAYS AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
TWO C1-LIKE AND ONE V-LIKE DOMAINS.
DR EMBL: D87968; BAA13521.1; -.
DR EMBL: D87967; BAA13520.1; -.
DR EMBL: U89694; AAB92591.1; -.
DR EMBL: AF072543; AAC24886.1; -.
DR EMBL: AF072544; AAC24887.1; -.
DR MGD: MGI:108563; Ptpns1.
DR PFM: PFM0047; Ig: 3.
KW Signal; Transmembrane; Alternative splicing; Immunoglobulin domain;

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KM	Glycoprotein:	SH3-binding:	Phosphorylation.
FT	SIGNAL	1	31
FT	CHAIN	32	513
FT	DOMAIN	32	373
FT	TRANSMEM	374	394
FT	DOMAIN	395	513
FT	DOMAIN	51	124
FT	DOMAIN	167	234
FT	DOMAIN	270	336
FT	DOMAIN	440	443
FT	DOMAIN	450	456
FT	DOMAIN	464	467
FT	DOMAIN	481	484
FT	DOMAIN	505	508
FT	MOD_RES	423	423
FT	MOD_RES	440	440
FT	MOD_RES	464	464
FT	MOD_RES	481	481
FT	MOD_RES	505	505
FT	CARBOHYD	54	54
FT	CARBOHYD	92	92
FT	CARBOHYD	168	168
FT	CARBOHYD	180	180
FT	CARBOHYD	205	205
FT	CARBOHYD	209	209
FT	CARBOHYD	246	246
FT	CARBOHYD	271	271
FT	CARBOHYD	293	293
FT	CARBOHYD	302	302
FT	CARBOHYD	312	312
FT	CARBOHYD	320	320
FT	CARBOHYD	345	345
FT	CARBOHYD	367	367
FT	VARSPLIC	147	364
FT	VARSPLIC	425	428
FT	CONFLICT	10	10
FT	CONFLICT	29	29
FT	CONFLICT	67	67
FT	CONFLICT	74	74
FT	CONFLICT	83	83
FT	CONFLICT	86	87
FT	CONFLICT	90	90
FT	CONFLICT	91	91
FT	CONFLICT	96	96
FT	CONFLICT	114	114
FT	CONFLICT	118	118
FT	CONFLICT	126	127
FT	CONFLICT	128	128
FT	CONFLICT	194	194
FT	CONFLICT	224	224
FT	CONFLICT	351	351
FT	CONFLICT	365	365
FT	CONFLICT	490	490
SO	SEQUENCE	513 AA;	56425 MW; DP29251A CRC32;
Query Match	Similarity	13.1%;	Score 124; DB 11; Length 513;
Best Local	Similarity	28.4%;	Pred. No. 8.91e-07;
Matches	Conservative	29;	Mismatches 32; Indels 10; Gaps 10;
Db	27	TGYTGKELKATQPEKSVSYAAGDSIVLCITL-SLL-P-V-GP-IKWYRG-VGQS-RLLI	79
QY	16	SGTGG-DIVLVQSPDSLAVSLGERATIKCSKSSOSILNSRTRENTLAYWQRGPCKPLLI	74
Db	80	YSFTEGHPRPTVYNSDATKRNNMPSEISINVTPEADGATYYC	121
QY	75	Y-WASTRESGVPPDRFSGS-G-SCDTDFLTLLISSQLADVAAYVIC	114

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ID RESULT 5 PRELIMINARY: PRT: 122 AA.
AC Q99604.
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE TRGV9. (FRAGMENT).
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LEFRANC M.P.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE; 90033295.
RX DARIAVACH P., LEFRANC M.P.;
RT "The promoter regions of the T-cell receptor V9 gamma (TRGV9) and V2
RT delta (TRVD2) genes display short direct repeats but no TATA box.";
RL FEBS Lett. 226:185-191(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA LEFRANC M.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; X15774; CAA3345.1; -.
DR HSSP; P80362; IWTL.
DR PFAM; PF00047; I9; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13441 MW; C07D3DB9 CRC32;

Query Match 13.0%; Score 123; DB 4; Length 122;
Best Local Similarity 37.1%; Pred. No. 1.36e-05;
Matches 23; Conservative 16; Mismatches 16; Indels 7; Gaps 6

Db 117 CA 118
QY 114 CT 115

RESULT 6 PRELIMINARY: PRT: 122 AA.
AC Q99603.
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE TRGV9. (FRAGMENT).
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 88283640.
RX HUCK S., DARIAVACH P., LEFRANC M.P.;
RT "Variable region genes in the human T-cell rearranging gamma (TRG)
RT locus: V-J junction and homology with the mouse genes.";
RL EMBO J. 7:719-726(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA LEFRANC M.P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; X07205; CAA30181.1; -.
DR HSSP; P80362; IWTL.
DR PFAM; PF00047; I9; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13414 MW; E1CCA59F CRC32;

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Query Match 13.0%; Score 123; DB 4; Length 122;
 Best Local Similarity 37.1%; Pred. No. 1,36e-06;
 Matches 23; Conservative 16; Mismatches 16; Indels 7; Gaps 6;

DB 57 WYREGEVIOFLVSIYDGYAKESGIPSGKFEVDRIPTSTLTITINHEKODIATY 116
 117 CA 118
 114 CT 115

Query Match 12.7%; Score 120; DB 6; Length 210;
 Best Local Similarity 27.2%; Pred. No. 4.80e-06;
 Matches 37; Conservative 32; Mismatches 56; Indels 11; Gaps 9;

DB 2 QPGLWLLATQALALRGSSVLAQPGSVVYQTNQVIMSCAATSP-TS-TRIYWL-RHR 58
 4 QAOVLLILLWVGTCGDIVLTQSPDLAVSLGERATISCKSSQSLNSTRRENYLAWYQ 63
 59 QASPSDSHECLAYNPDKIGIVYGOVEPEKLVFPDATSIILNLSYKADSGIYFCMT 118
 64 QKQKPGPKL-LIYMASTR-S-G--V-PDRFSGSGSGDFTLTISLSLAQEDVAVYYC-T 115
 119 VGSPELLFGKGRPLSY 134
 116 QSYNLYTFGOGTKVEI 131

RESULT 8
 ID 09WNT4 PRELIMINARY; PRT: 509 AA.
 AC 09WNT4;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
 DE BIT.
 GN BIT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RA, SEQUENCE FROM N.A.

RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RA SANO S.;
 RT "Mouse type III RT."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB018194; BAA76555.1; -
 SQ SEQUENCE 509 AA; 55986 MW; 34F9E651 CRC32;

Query Match 12.6%; Score 119; DB 11; Length 509;
 Best Local Similarity 27.5%; Pred. No. 7.29e-06;
 Matches 28; Conservative 32; Mismatches 32; Indels 10; Gaps 10;

DB 27 TGATGKELKVTQPKSVSYAAGSTVNLCTLT-SLL-P-V-GP-IRWRG-VG-PSRLTI 79
 16 SGTGCG-DIVLTQSPDLAVSLGERATISCKSSQSLNSTRRENYLAWYQKPGPKLLI 74
 80 YSFAGEYVPRINVDSTTKRNMDFSIKSNYTPADAGIYIC 121
 75 Y-WASTRESGVDPDRSGSG-SGTDEFTLTISLSLAQEDVAVYYC 114

Query Match 12.5%; Score 118; DB 4; Length 81;
 Best Local Similarity 38.8%; Pred. No. 1.10e-05;
 Matches 19; Conservative 11; Mismatches 16; Indels 3; Gaps 3;

DB 33 AVQGRFAISRDNKNSLYLQISGLAEDTAVYYCARVLN-YRPNQMDV 80
 83 GVPDRFS-GSGSGTD-FTLTISLSLAQEDVAVYYCTQSYNLYTFGOGTKV 129

RESULT 10
 ID 095973 PRELIMINARY; PRT: 150 AA.
 AC 095973;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, last annotation update)
 DE VH4 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
 GN IGM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RA SEQUENCE FROM N.A.
 RA SUH C.-H., SONG C.-H., LEE C.-H., LEE S.-K.;
 RT "Clonal proliferation of IGM secreting B cell in the synovium of
 RT Behcet's patient with arthritis."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF105795; AAC79084.1; -
 DR HSSP; P01825; 7FAB.
 KW SIGNAL.
 FT SIGNAL. 1 19 POTENTIAL.

FT	CHAIN	20	>150	WH4 HEAVY CHAIN VARIABLE REGION.
FT	NON TER	150	150	
SO	SEQUENCE	150 AA;	16315 MW;	508A92A6 CRC32;
Query Match				
	Best Local Similarity	39.1%;	Pred. No. 8,58e-05;	
	Matches	18;	Conservative	12;
			Mismatches	14;
			Indels	2;
			Gaps	2
Db	90 ISVDTSKNOFSLRSSVTADTVAYTCARLQMGAFDENGHGTMTV	135		
Oy	88 FSGSGSGTDFLTLLISLQAEDEVAYVYCTQ-SYNYLYTF-GGGTKVEI	131		
RESULT 11				
ID	Q13970	PRELIMINARY;	PRT;	198 AA.
AC	Q13970:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE	CD8 ANTIGEN.			
GN	CD8A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89215302.			
RA	NORMENT A.M., LONBERG N., LACY E., LITTMAN D.R.;			
RT	"Alternatively spliced mRNA encodes a secreted form of human CD8 alpha. Characterization of the human CD8 alpha gene.";			
RL	J. Immunol. 142:3312-3319(1989).			
DR	EMBL; M26315; AAA79218.1;			
DR	EMBL; M26313; AAA79218.1; JOINED.			
DR	HSSP; P01732; 1CD8.			
DR	PFAM; PF00047; 1g. 1.			
SO	SEQUENCE 198 AA; 21585 MW; B8399CB1 CRC32;			
Query Match				
	Best Local Similarity	28.7%;	Pred. No. 8,58e-05;	
	Matches	25;	Conservative	27;
			Mismatches	24;
			Indels	11;
			Gaps	11
Db	44 OVLNSNPTS-GC-SWLFPPGGAASPTLLYLSONKPKAEGDLOFGSKRLDDTVLT	101		
Oy	47 OSLMSRRENTLAN-YQOK-PGQPPKLLIYWA-ST-RES-GV-PDRFSGSGSGTDFLT	100		
Db	102 LSDFERNEGYYFCALSNSIMY-FSH	127		
Oy	101 ISSLQAEDEVAYVYCTQ-SYN-LYTFGQ	125		
RESULT 12				
ID	O9XSM6	PRELIMINARY;	PRT;	235 AA.
AC	O9XSM6:			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	CD8 ALPHA CHAIN PRECURSOR.			
OS	Salimiri sciureus (Common squirrel monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salimiri.			
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-92039;			
RX	MEDLINE; 99299362.			
RA	URETA-VIDL A., GARCIA Z., LEWONNIER F.A., KAZANI M.;			
RT	"Molecular characterization of cDNAs encoding squirrel monkey (Salimiri sciureus) CD8 alpha and beta chains.";			
RL	Immunogenetics 49:718-721(1999).			
DR	EMBL; AJ130818; CABA1462.1;			
KM	Signal.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	235	CD8 ALPHA CHAIN.

SO	SEQUENCE	235 AA;	25728 MM;	F22E0AB5 CRC32;	
	Query Match	12.0%;	Score 113;	DB 6;	Length 235;
	Best Local Similarity	29.0%;	Pred. No. 8,58e-05;		
	Matches	18;	Conservative	19;	Mismatches 19; Indels 6; Gaps 6;
Db	55 SWLQKRCGAASPFELLYISOTKRXVADGDLDAQKFSGKMGKSDSITLLRDFRFDGCFYF	114			
OY	60 AM-YQOK-PGQPKLLIY-WAST-R-ESGV-PDRFSSGSGGTFTLLISSIQADVAVY	113			
Db	115 CS	116			
OY	114 CT	115			
RESULT	13				
ID	O9Y2N4	PRELIMINARY;	PRT;	169 AA.	
AC	O9Y2N4;				
DT	01-NOV-1999 (TReMBLrel. 12, Created)				
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)				
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)				
DE	T-CELL RECEPTOR V-GAMMA 8.				
GN	H.NH1021A08.4.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE: 99063792.				
RA	SULSTON J.E., WATERSTON R.;				
RT	"toward a complete human genome sequence.";				
RL	Genome Res. 8:1097-1108(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	ARNETT C., MOHLMANN P., LE T.;				
RT	"The sequence of Homo sapiens BAC clone NH0121A08.";				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	WATERSTON R.H.;				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	WATERSTON R.;				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AC006033; AAD15555.1; -.				
KW	Receptor.				
SO	SEQUENCE	169 AA;	18958 MM;	DD061B665 CRC32;	
	Query Match	11.8%;	Score 111;	DB 4;	Length 169;
	Best Local Similarity	29.2%;	Pred. No. 1.92e-04;		
	Matches	19;	Conservative	20;	Mismatches 19; Indels 7; Gaps 5;
Db	50 YTHWTLHDEGAAPORLLYDYSNRVLESGISREKHYATYATGSKLFTIENTIERPDSG	109			
OY	58 YLAWQCKPGQGP-KLLIYMA-STR--ESGVP-DRESG-SGSETDFTLLISSIQADVA	110			
Db	110 VYCA	114			
OY	111 VYCT	115			
RESULT	14				
ID	O75736	PRELIMINARY;	PRT;	81 AA.	
AC	O75736;				
DT	01-NOV-1998 (TReMBLrel. 08, Created)				
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)				
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)				
DE	IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).				
GN	VI.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.				

 (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 7 19:03:42 2000; Maspar time 9.71 Seconds

Tabular output not generated. 322.033 Million cell updates/sec

Title: >US-09-249-011-8
 Description: (1-132) from US09249011.pep
 Perfect Score: 943
 Sequence: 1 MDSQAOVLILLILMWSGTCG.....YCTOSINLYTFFGQKVEIK 132

Scoring table:
 PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq36
 l-geneseqp

Statistics: Mean 30.911; Variance 170.801; scale 0.181

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	819	86.9	148	1	P93078	1.28e-51
2	818	86.7	239	1	R76087	1.52e-51
3	803	85.2	137	1	W10545	2.11e-50
4	797	84.5	137	1	W10544	6.05e-50
5	777	82.4	133	1	R59509	2.01e-48
6	770	81.7	133	1	P80894	6.85e-48
7	768	81.4	134	1	W06206	9.12e-48
8	762	80.8	133	1	R85909	2.78e-47
9	756	80.2	241	1	R28809	7.94e-47
10	751	79.6	137	1	W10547	1.90e-46
11	748	79.3	133	1	R48633	3.22e-46
12	744	78.9	137	1	W21655	6.47e-46
13	744	78.9	139	1	R99469	6.47e-46
14	743	78.8	134	1	R30485	7.71e-46
15	741	78.6	137	1	W21653	1.09e-45
16	737	78.2	134	1	R25158	2.20e-45
17	731	77.5	134	1	R38317	6.28e-45
18	698	74.0	133	1	R59511	2.00e-42
19	697	73.9	495	1	Y06908	2.38e-42
20	697	73.9	495	1	W32480	2.38e-42
21	693	73.5	134	1	R81838	4.78e-42
22	691	73.3	134	1	R81841	6.77e-42
23	686	72.7	155	1	Y06912	1.62e-41

ID	Score	Query Match	Length	ID	Description	Pred. No.
24	686	72.7	155	1	W22483	1.62e-41
25	686	72.7	342	1	Y06909	1.62e-41
26	686	72.7	342	1	W22482	1.62e-41
27	683	72.4	131	1	R55553	2.73e-41
28	676	71.7	171	1	R30144	9.25e-41
29	676	71.7	171	1	R38320	9.25e-41
30	676	71.7	274	1	R38319	9.25e-41
31	676	71.7	284	1	R38321	9.25e-41
32	675	71.6	113	1	R50314	1.10e-40
33	673	71.4	113	1	W27346	1.56e-40
34	668	70.8	113	1	R50313	3.73e-40
35	666	70.6	285	1	R48638	5.28e-40
36	665	70.5	114	1	Y06830	6.28e-40
37	664	70.4	219	1	R76086	8.90e-40
38	663	70.3	249	1	W60770	8.90e-40
39	660	70.0	133	1	R55555	1.50e-39
40	660	70.0	288	1	W82743	1.50e-39
41	660	70.0	673	1	W82742	1.50e-39
42	659	69.9	111	1	R52059	1.79e-39
43	654	69.4	114	1	R45605	4.26e-39
44	654	69.4	114	1	W15537	4.26e-39
45	648	68.7	120	1	R61240	1.21e-38

ALIGNMENTS

RESULT 1
 ID P93078 standard; peptide; 148 AA.
 AC P93078;
 DT 14-MAR-1990 (first entry)
 DE Light chain of monoclonal antibody 6A4.
 KW Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
 PN EP-338395-A.
 PD 25-OCT-1989.
 PE 12-APR-1989; 106463.
 PR 19-APR-1988; DE-813023.
 PA (BEHW) Behringwerke.
 PI Domdey H, Marget M, von Specht BU;
 DR WPI: 89-310861/43.
 DR N-PSDB; N91603.
 PT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for P variable antibody regions.
 PS Claim 1; page 6; 7pp; german.
 CC The peptide is encoded by the light chain of monoclonal antibody 6A4.
 CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa. It is used for therapy and diagnosis of infection, and as a carrier for drugs. The antibody is IgG2a subclass.
 SQ Sequence 148 AA;

Query Match 86.9%; Score 819; DB 1; Length 148;
 Best Local Similarity 86.4%; Pred. No. 1.28e-51;
 Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

ID	Score	Query Match	Length	ID	Description	Pred. No.
Db	1	MDSQAOVLILLILMWSGTCGDIIVLQSPDSLAVSAGERATISCSGSLNSRTRENTLA	60			
Qy	1	MDSQAOVLILLILMWSGTCGDIIVLQSPDSLAVSAGERATISCSGSLNSRTRENTLA	60			
Db	61	WYQKPGQSPKLLIYWASTRESGVDPDRFTSGSGTDFTLTISVQAEDLAVYCKOSYNTL	120			
Qy	61	WYQKPGQSPKLLIYWASTRESGVDPDRFTSGSGTDFTLTISVQAEDLAVYCKOSYNTL	120			
Db	121	RTFGGKTLK 132				
Qy	121	RTFGGKTLK 132				

RESULT 2
 ID R76087 standard; protein; 239 AA.
 AC R76087;
 DT 21-NOV-1995 (first entry)
 DE Mab 55.1 light chain.
 KW Antigen binding structure; complementarily determining region; CDR; CA5.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW	monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;
KW	transgenic animal; transgenic plant; antibody engineering;
KW	humanized antibody; immunotoxin.
OS	Mus sp.
PH	Key
FT	peptide
FT	1..20
FT	/label= Sig_peptide
FT	21..239
FT	/label= Mat.protein
FT	/note= "claim 3, page 98"
PN	WO9515382-A.
PD	08-JUN-1995.
PF	29-NOV-1994. G02610.
PR	03-DEC-1993; GB-024819.
PR	03-JUN-1994; GB-011089.
PA	(ZENE) ZENECA LTD.
PI	Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
PI	Rose MS, Wright AF.
DR	WPI: 95-215262/28.
DR	N-PSDB: 094036.
PT	Antigen binding structures containing CDRs recognising the CA55.1
PT	antigen - produced by hybridomas and host cells, for use in the
PT	diagnosis and therapy of cancer
PS	Disclosure; Fig.16; 121pp; English.
CC	Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
CC	antigen CA55.1. cDNAs for the heavy (094037) and light (094036)
CC	chains of 55.1 were isolated, and Fabab', Fabab'2, Fdb, scFv or
CC	V-chain humanised 55.1 constructs have been expressed in myeloma
CC	cells and E. coli.
CC	Sequence 239 AA;
90	

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Query Match      86.7%; Score 818; DB 1; Length 239;
Best Local Similarity 84.8%; Pred. No. 1,52e-51;
Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Db      1 MDSQAOVLILLLWVSGICGDIVMSQSPSSSLAVSAGEKVTWMSCKSSQSLNSRTRKNLYLA 60
Oy      1 MDSQAOVLILLLWVSGICGDIVLTQSPDLSLAVSLGERATISSCKSSQSLNSRTRKNLYLA 60

Db      61 WYQARPGCSPLLLIYMASTRSGVPPDRRTGSGSDTDLTITSSVQADLAIIYCKOSYTL 120
Oy      61 WYQARPGCPPLLLIYMASTRSGVPPDRPSGSGSDTDLTITSSVQADVAIVYCTOSYTL 120

Db      121 RTFGGRTKLEIK 132
Oy      121 YTFGGRTKVEIK 132

RESULT      3
ID      W10545 standard; Protein; 137 AA.
AC      W10545;
DT      25-SEP-1997 (first entry)
DE      Humanised murine anti-E-selectin antibody Cyt188(UB).
KW      Humanised; murine; mouse; E-selectin; antibody; light chain;
KW      variable region; detection; inhibition; mediation; cell adhesion;
KW      diagnosis; reduction; inflammation; septic shock; AIDS; sepsis;
KW      acute respiratory distress syndrome; genetic disease; breast disease;
KW      cancer; treatment; splanchnic occlusion shock; poritiasis;
KW      complement; chimeric.
OS      Chimeric - Mus spp.
OS      Chimeric - Homo sapiens.
OS      Synthetic.
PN      W03640342.AL.
PD      19-DEC-1996.
PF      06-JUN-1996; U09204.
PR      07-JUN-1995; US-482112.
PA      (CYTE-) CYTEL CORP.
PI      Bendig MM, Jones SR, Perez C, Saldanha JW, Williams MA,
PI      Jones S;
PI      WPI: 97-077272/07.
DR      W10545DB; T60730.
DE      Humanised anti-E-selectin antibody - useful for diagnosis and
DE      treatment of, e.g. inflammatory responses, septic shock, acute

```

PT respiratory distress syndrome or cancer
PS Claim 18; Page 71; 89pp; English.
CC The present sequence is the humanised murine anti-E-selectin
CC antibody (Ab) light chain variable region, CY1788V(LB). The Ab can
CC be used to detect E-selectin, or inhibit E-selectin mediated cell
CC adhesion. It can also be used to diagnose, reduce or inhibit an
CC inflammatory response, or the severity of pathologies, e.g. septic
CC shock, acute respiratory distress syndrome, wound associated
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
CC sphincteric occlusion shock, or psoriasis. It can be administered to
CC a human without inducing an immune response, in addition, the
CC effector portion of the Ab can interact with various components of
CC the human immune system, including complement.
SQ Sequence 137 AA; 1

[illegible]

	RESULT	4	
ID	W10544 standard; Protein; 137 AA.		
AC	W10544;		
DT	25-SEP-1997 (first entry)		
DE	Humanised murine anti-E-selectin antibody Cy1788V(LA).		
KM	Humanised; murine; mouse; E-selectin; antibody; light chain;		
KM	variable region; detection; inhibition; mediation; cell adhesion;		
KM	diagnosis; reduction; inflammation; septic shock; AIDS; sepsis;		
KM	acute respiratory distress syndrome; gross cystic breast disease;		
KM	cancer; treatment; splanchic occlusion shock; psoriasis;		
KW	complement; chimeric		
OS	Chimeric - Mus spp.		
OS	Chimeric - Homo sapiens.		
PN	Synthetic.		
PN	WO9640942-A1.		
PD	19-DEC-1996.		
PF	06-JUN-1996; UO9204.		
PR	07-JUN-1995; US-482112.		
PA	(CYTE-) CYTEL CORP.		
P1	Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;		
P1	Jones SJ		
DR	WPI; 97-077272/07.		
DR	N-PSDB; T60729.		
PT	Humanised anti-E-selectin antibody - useful for diagnosis and		
PT	treatment of e.g. inflammatory responses, septic shock, acute		
PT	respiratory distress syndrome or cancer		
PT	Claim 17; Page 69; 89pp; English.		
CC	The present sequence is the humanised murine anti-E-selectin		
CC	antibody (Ab) light chain variable region, Cy1788V(LA). The Ab can		
CC	be used to detect E-selectin, or inhibit E-selectin mediated cell		
CC	adhesion. It can also be used to diagnose, reduce or inhibit an		
CC	inflammatory response, or the severity of pathologies, e.g. septic		
CC	shock, acute respiratory distress syndrome, wound associated		
CC	sepsis, gross cystic breast disease or cancer, or treat, e.g.		
CC	splanchnic occlusion shock, or psoriasis. It can be administered to		
CC	a human without inducing an immune response. In addition, the		
CC	effector portion of the Ab can interact with various components of		
CC	the human immune system, including complement.		
SO	Sequence 137 AA;		

Query	Subject	Score	Length	Ident	Positives	Score	Length	Ident	Positives
1	1	100.0	100	100	100	100.0	100	100	100
2	2	99.9	100	100	100	99.9	100	100	100
3	3	99.8	100	100	100	99.8	100	100	100
4	4	99.7	100	100	100	99.7	100	100	100
5	5	99.6	100	100	100	99.6	100	100	100
6	6	99.5	100	100	100	99.5	100	100	100
7	7	99.4	100	100	100	99.4	100	100	100
8	8	99.3	100	100	100	99.3	100	100	100
9	9	99.2	100	100	100	99.2	100	100	100
10	10	99.1	100	100	100	99.1	100	100	100
11	11	99.0	100	100	100	99.0	100	100	100
12	12	98.9	100	100	100	98.9	100	100	100
13	13	98.8	100	100	100	98.8	100	100	100
14	14	98.7	100	100	100	98.7	100	100	100
15	15	98.6	100	100	100	98.6	100	100	100
16	16	98.5	100	100	100	98.5	100	100	100
17	17	98.4	100	100	100	98.4	100	100	100
18	18	98.3	100	100	100	98.3	100	100	100
19	19	98.2	100	100	100	98.2	100	100	100
20	20	98.1	100	100	100	98.1	100	100	100
21	21	98.0	100	100	100	98.0	100	100	100
22	22	97.9	100	100	100	97.9	100	100	100
23	23	97.8	100	100	100	97.8	100	100	100
24	24	97.7	100	100	100	97.7	100	100	100
25	25	97.6	100	100	100	97.6	100	100	100
26	26	97.5	100	100	100	97.5	100	100	100
27	27	97.4	100	100	100	97.4	100	100	100
28	28	97.3	100	100	100	97.3	100	100	100
29	29	97.2	100	100	100	97.2	100	100	100
30	30	97.1	100	100	100	97.1	100	100	100
31	31	97.0	100	100	100	97.0	100	100	100
32	32	96.9	100	100	100	96.9	100	100	100
33	33	96.8	100	100	100	96.8	100	100	100
34	34	96.7	100	100	100	96.7	100	100	100
35	35	96.6	100	100	100	96.6	100	100	100
36	36	96.5	100	100	100	96.5	100	100	100
37	37	96.4	100	100	100	96.4	100	100	100
38	38	96.3	100	100	100	96.3	100	100	100
39	39	96.2	100	100	100	96.2	100	100	100
40	40	96.1	100	100	100	96.1	100	100	100
41	41	96.0	100	100	100	96.0	100	100	100
42	42	95.9	100						

FT	region	21..133
FT		/label=V region of L chain
FN	Ep-270077-A.	
PD	08-JUN-1988.	
PF	01-DEC-1987; 117760.	
PR	03-DEC-1986; JP-288340.	
PR	26-NOV-1987; JP-298513.	
PA	(SOMO) Sumitomo Chem Ind K.	
PI	Nakatani T, Momura N, Horigome K, Noguchi H.;	
DR	WPI; 88-156310/23.	
DR	N-PSDB: N80499.	
PT	New gene encoding for antibody to <i>Pseudomonas aeruginosa</i> exotoxin -	
PT	plus recombinant vectors and host cells, useful for treating	
PT	infections.	
PS	Claim 4; page 25; 39pp; English.	
CC	Sequence is variable region of light chain of anti-exotoxin	
CC	antibody with signal sequence. N80498 encodes the same sequence	
CC	except that its signal peptide-encoding sequence contains an	
CC	intron.	
CC	See also N80495-N80496, N80498 and N80941-2.	
SC	Sequence 133 AA;	
SC		
Query Match	81.7%; Score 770; DB 1; Length 133;	
Best Local Similarity	83.5%; Pred. No. 6,85e-48;	
Matches 111; Conservative	8; Mismatches 13; Indels 1; Gaps 1	
Db	1 MYLQYVFISLLWISGAVGDIWMTQSPHSDSLAVSLGERATINCKSSQSVLYSSNNKNYLA 60	
Qy	1 MDSQAQVILILLWVSGCGDIVLTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNTRENYLA 60	
Db	61 WYQKPGQPKLLIYWASTRESSGVPDFRSGSGSGTDFLTITISLQAEDVAVYYCQYYST 120	
Qy	61 WYQKPGQPKLLIYWASTRESSGVPDFRSGSGSGTDFLTITISLQAEDVAVYYCTQSYNL 120	
Db	121 PRTFGCGTKVEIK 133	
Qy	121 YTFEGGTKVEIK 132	
RESULT	7	
ID	W06206 standard; Protein; 134 AA.	
AC	W06206;	
DT	17-FEB-1997 (first entry)	
DE	Xenograft antibody HAR-1 kappa light chain variable region.	
KW	Xenograft rejection; xenotransplantation; organ transplant;	
KW	animal model; hamster; monoclonal antibody; HAR-1.	
OS	Rattus sp.	
FT	Key	Location/Qualifiers
FT	region	1..20
FT	region	/label=Leader
FT	region	21..43
FT	region	/label=FR-1
FT	region	/note="framework region 1"
FT	region	44..60
FT	region	/label=CDR-1
FT	region	/note="complementarity determining region 1"
FT	region	61..75
FT	region	/label=FR-2
FT	region	/note="framework region 2"
FT	region	76..82
FT	region	/label=CDR-2
FT	region	/note="complementarity determining region 2"
FT	region	83..114
FT	region	/label=FR-3
FT	region	/note="framework region 3"
FT	region	115..122
FT	region	/label=CDR-3
FT	region	/note="complementarity determining region 3"
FT	region	123..134
FT	region	/label=FR-4
FT	region	/note="framework region 4"
FN	W09636358-A1.	
PD	21-NOV-1996.	

CC was used to transform *E. coli* JA221(Iq) to ampicillin resistance.
 CC pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was
 CC ligated into NotI linearised pSAB132 which had been dephosphorylated
 CC by calf alkaline phosphatase. This generates the plasmid pMDR1007.
 CC The dephosphorylated mixture was fractionated through low temperature
 CC melting agarose and used to transform *E. coli* JA221(Iq) to ampicillin
 CC resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
 CC order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
 CC 1-AA112 of the humanised 5A8 light chain variable region (LV) followed
 CC by genomic DNA encoding AA108-AA214 of the human kappa light chain,
 CC ie, the light chain constant region (LC). This polypeptide is an
 CC antibody homolog which was shown to bind to CD4 but did not block the
 CC binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
 CC lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
 CC syncytia formation. This homolog can be used in the detection,
 CC prophylaxis and treatment of diseases caused by infective agents whose
 CC primary targets are CD4+ cells.
 S0 Sequence 241 AA;

Query Match 80.2%; Score 756; DB 1; Length 241;
 Best Local Similarity 81.8%; Pred. No. 7,94e-47;
 Matches 108; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Db 3 MRVPAQLGLLLWPGAGDIWMTQSPDSLAVSLGERATINCKSSGSLVSTNKNYLA 62
 1 MDSQAOVLILLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLA 60
 Qy 63 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQYYSY 122
 61 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQSYNL 120
 Qy 61 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQSYNL 120
 Db 123 RTFGGTRKVEIK 134
 121 YTFGGTRKVEIK 132
 Qy 121 YTFGGTRKVEIK 132

RESULT 10
 ID W10547 standard; Protein; 137 AA.
 AC W10547;
 DT 25-SEP-1997 (first entry)
 KW Humanised; murine; mouse; E-selectin; antibody; light chain;
 KW variable region; detection; inhibition; mediation; cell adhesion;
 KW diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
 KW acute respiratory distress syndrome; gross cystic breast disease;
 KW cancer; treatment; splanchic occlusion shock; psoriasis;
 KW complement.
 OS Mus spp.
 PN M09640942-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U092004.
 PR 07-JUN-1995; US-482112.
 PA (CYTE-) CYTEL CORP.
 PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;
 PI Jones S;
 PI WPI: 97-077272/07.
 DR N-PSDB: T60734.
 PT Humanised anti-E-selectin antibody - useful for diagnosis and
 PT treatment of, e.g. inflammatory responses, septic shock, acute
 PT respiratory distress syndrome or cancer
 PS Example II: Page 55; 89pp; English.
 CC The present sequence is the wild type murine anti-E-selectin
 CC antibody (Ab) light chain variable region, CY1787(L), which was
 CC used in the preparation of the humanised anti-E-selectin Ab light
 CC chain variable regions, CY1788V(LA-B). The humanised Ab can
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell
 CC adhesion. They can also be used to diagnose, reduce or inhibit an
 CC inflammatory response, or the severity of pathologies, e.g. septic
 CC shock, acute respiratory distress syndrome, wound associated
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.
 CC splanchic occlusion shock, or psoriasis. They can be administered
 CC to a human without inducing an immune response, in addition, the
 CC effector portion of the Ab can interact with various components of

CC the human immune system, including complement.
 S0 Sequence 137 AA;

Query Match 79.6%; Score 751; DB 1; Length 137;
 Best Local Similarity 76.7%; Pred. No. 1.90e-46;
 Matches 102; Conservative 17; Mismatches 13; Indels 1; Gaps 1;

Db 5 MESQGVMSLLFWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLA 64
 1 MDSQAOVLILLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLA 60
 Qy 65 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQYYSY 124
 61 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQSYNL 120
 Db 125 PLTFGAGTRKVEIK 137
 121 YTFGGTRKVEIK 132
 Qy 121 YTFGGTRKVEIK 132

RESULT 11
 ID R48633 standard; Protein; 133 AA.
 AC R48633;
 DT 02-SEP-1994 (first entry)
 DE Sequence of Hum4VL gene ClaI-HindIII segment in pRL1001
 KW Antibody; Hum4VL; variable light; single chain Fv immunoglobulin.
 OS Synthetic.

FH Key Location/Qualifiers
 FT peptide 1..20
 FT protein 21..133
 FT region 44..47
 FT region 76..82
 FT region /label= CDR2
 FT region 115..123
 FT /label= CDR3

PN M09404691-A.
 PD 03-MAR-1994.
 PF 20-AUG-1993; U07918.
 PR 21-AUG-1992; US-935695.
 PA (DMC) DOW CHEM CO.
 PI Afholter JA, Kotite NJ, Mezes PS, Richard RA;
 PI WPI: 94-083206/10.
 DR N-PSDB: Q56735.
 PT Dimer and multimer forms of single chain antibody polypeptide(s)
 PT - used in vivo and in vitro in diagnostics, therapy, imaging and
 PT bio-sensors
 PS Example; Fig 5; 99pp; English.
 CC Hum4VL was obt. by PCR DNA amplification using pRL1001 as a
 CC template and oligos UNH1 and UNH2(-) as primers. The DNA sequence
 CC in pRL1001 coding for the Hum4VL is given in Q56735, and the
 CC AA sequence it encodes in R48633. Human C-kappa is found to the 3'
 CC end of the coding strand of Q56735.
 S0 Sequence 133 AA;

Query Match 79.3%; Score 748; DB 1; Length 133;
 Best Local Similarity 81.2%; Pred. No. 3.22e-46;
 Matches 108; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Db 1 WYLQGVFISLLWVSGTGDIVLTQSPDSLAVSLGERATINCKSSQSLVSSNNKNYLA 60
 1 MDSQAOVLILLWVSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENTLA 60
 Qy 61 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQYYSY 120
 61 WYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSSLOAEDEVAYVYCCQSYNL 120
 Db 121 PLTFGAGTRKVEIK 133
 121 YTFGGTRKVEIK 132
 Qy 121 YTFGGTRKVEIK 132

RESULT 12
 ID W21655 standard; Protein; 137 AA.

PF 17-JUN-1992; 110262.
 PR 18-JUN-1991; KR-010040.
 PR 06-FEB-1992; KR-001692.
 PR 04-MAY-1992; KR-007593.
 PA (KOAD) KOREA ADV INST SCI & TECHN.
 PI Chung HK, Han MH, Hong HJ, Jin BR, Park SS, Ryu CJ;
 DR N-PSDB; Q34842.
 WPI: 93-001907/01.
 CC Chimaeric antibody specific for hepatitis B virus pre-S2 surface
 PT antigen - useful for treating and preventing hepatitis B virus
 PT infections
 PS Claim 3; Page 12; 23pp; English.
 CC This sequence represents that of the V kappa region of a chimaeric
 CC human/murine monoclonal antibody to the pre-S2 antigen. The pre-S2
 CC antigen is reported to have enhanced immunogenicity as compared with
 CC the currently used S antigen. Use of the human C region eliminates
 CC patient immune response to the murine C region which improves
 CC efficacy and reduces undesirable clinical side effects.
 SQ Sequence 134 AA;

Query Match 78.8%; Score 743; DB 1; Length 134;
 Best Local Similarity 78.9%; Pred. No. 7,71e-46;
 Matches 105; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

Db 1 MDSQAOVLMLLLWVSGTCDIVMSQSPSSLAIVSGEKVTMCKSSQSLYSSNQNTLA 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 1 MDSQAOVLMLLLWVSGTCDIVLQSPDLSLAVSLGERATISCKSSQSLNRTRENTLA 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 WYQKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITISSVKAEDPAVYTCQY 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 WYQKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITISSVKAEDPAVYTCQY 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 121 PSTFGGTYLEIK 133
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 -YTFGGTKVEIK 132

RESULT 15
 ID W21653 standard; Protein; 137 AA.
 AC W21653;
 DT 03-JAN-1998 (first entry)
 DE Mouse Mab 15 light chain variable region.
 KW Humanised antibody; monoclonal antibody; Mab 15; tumour;
 KW lung cancer; therapy.
 OS Mus musculus.
 FH Key Peptide
 FT 1. .24 Location/Qualifiers
 FT /label= Sig_peptide
 FT 25. .138
 FT /label= Mat_protein
 FT 25. .47
 FT /label= Framework-1
 FT 48. .63
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT 64. .79
 FT /label= Framework-2
 FT 80. .86
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT 87. .118
 FT /label= Framework-3
 FT 119. .126
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT 128. .137
 FT /label= Framework-4
 FT Region
 FT EP-781847-A1.
 PN 02-JUL-1997.
 PD 25-OCT-1996; 117154.
 PR 06-NOV-1995; EP-117407.
 PR (MERE) MERCK PATENT GMBH.
 PI Bendig M, Jones T, Saldana J;

DR WPI: 97-334904/31.
 DR N-PSDB; T72238.
 PT Humanised form of murine monoclonal antibody Mab 15 - useful for
 PT treating lung cancer
 PS Claim 14; Fig 1; 71pp; English.
 CC This polypeptide comprises the light chain variable region VL
 CC of murine monoclonal antibody (mab) 15 (DSM ACC2117), a Mab that
 CC shows a therapeutic effect on human tumour cells, especially human
 CC lung cancer. Its sequence was deduced from an isolated cDNA
 CC clone (see T72238). The Mab 15 VH region sequence (W21654)
 CC has also been determined. Amplified VL and VH cDNA sequences were
 CC used in a claimed process for the production of novel humanised,
 CC reshaped Mab 15 having humanised, reshaped VL and VH regions (see
 CC W21651 and W21652), which can be used for treating tumours,
 CC especially lung cancer, and for the manufacture of a drug related
 CC to tumours, especially lung cancer.
 SQ Sequence 137 AA;

Query Match 78.6%; Score 741; DB 1; Length 137;
 Best Local Similarity 77.6%; Pred. No. 1.09e-45;
 Matches 104; Conservative 15; Mismatches 12; Indels 3; Gaps 2;

Db 5 MESHSLVTLMLLLWVSGTCDIVMSQSPSSLAIVSGEKVTMCKSSQSLYSSNQNTLA 64
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 1 MDSQAOVLMLLLWVSGTCDIVLQSPDLSLAVSLGERATISCKSSQSLNRTRENTLA 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 65 WYQKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITISSVKAEDPAVYTCQY 123
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 WYQKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITISSVKAEDPAVYTCQY 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 124 YPPTFGGTYLEIK 137
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 Y--TFGGTKVEIK 132

Search completed: Mon Aug 7 19:03:56 2000
 Job time : 14 secs.

W E R E H (TM)

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MSPICH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 7 19:05:17 2000; MasPar time 6.96 Seconds

Tabular output not generated. 273.659 Million cell updates/sec

Title: >US-09-249-011-8
Description: (1-132) from US09249011.pep
Perfect Score: 943
Sequence: 1 MDSQAQVLLILLMWSGTCG.....YCTQSYLYTFGGGTKEIK 132

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 28.955; Variance 168.930; scale 0.171

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	818	86.7	239	1	US-08-353-Sequence 37, Applicat	2.71e-49
2	756	80.2	241	2	US-07-816-Sequence 56, Applicat	8.21e-45
3	739	78.4	133	2	US-08-822-Sequence 12, Applicat	1.38e-43
4	733	77.7	133	4	PCT-US93-1-Sequence 2, Applicat	3.75e-43
5	711	75.4	133	4	PCT-US93-1-Sequence 2, Applicat	1.44e-41
6	698	74.0	133	4	PCT-US93-1-Sequence 9, Applicat	1.25e-40
7	697	73.9	155	3	US-08-828-Sequence 4, Applicat	1.47e-40
8	686	72.7	155	3	US-08-828-Sequence 11, Applicat	9.10e-40
9	686	72.7	342	3	US-08-828-Sequence 6, Applicat	9.10e-40
10	676	71.7	114	1	US-08-360-Sequence 6, Applicat	4.77e-39
11	676	71.7	114	2	US-09-017-Sequence 6, Applicat	4.77e-39
12	676	71.7	114	2	US-08-450-Sequence 6, Applicat	4.77e-39
13	676	71.7	114	2	US-09-014-Sequence 6, Applicat	4.77e-39
14	675	71.6	113	4	PCT-US93-0-Sequence 8, Applicat	5.63e-39
15	668	70.8	113	4	PCT-US93-0-Sequence 6, Applicat	1.79e-38
16	665	70.5	112	1	US-07-942-Sequence 30, Applicat	2.95e-38
17	654	70.4	219	1	US-08-353-Sequence 34, Applicat	3.48e-38
18	650	70.0	133	4	PCT-US93-1-Sequence 10, Applicat	6.74e-38
19	651	69.0	120	1	US-08-026-Sequence 4, Applicat	2.99e-37
20	646	68.5	265	2	US-08-403-Sequence 16, Applicat	6.83e-37
21	645	68.4	113	4	PCT-US93-1-Sequence 21, Applicat	8.05e-37
22	645	68.4	113	1	US-08-470-Sequence 21, Applicat	8.05e-37
23	645	68.4	113	1	US-08-667-Sequence 21, Applicat	8.05e-37

24	645	68.4	113	2	US-08-940-Sequence 21, Applicat	8.05e-37
25	645	68.4	113	1	US-08-467-Sequence 21, Applicat	8.05e-37
26	635	67.3	109	2	US-08-308-Sequence 23, Applicat	4.20e-36
27	621	65.9	147	2	US-08-860-Sequence 8, Applicat	4.24e-35
28	620	65.7	113	4	PCT-US93-1-Sequence 5, Applicat	5.01e-35
29	619	65.6	112	2	US-07-916-Sequence 15, Applicat	5.90e-35
30	608	64.5	282	2	US-08-860-Sequence 10, Applicat	3.63e-34
31	608	64.5	301	2	US-08-661-Sequence 14, Applicat	3.63e-34
32	608	64.5	553	2	US-08-661-Sequence 16, Applicat	3.63e-34
33	606	64.3	129	2	US-08-480-Sequence 4, Applicat	5.04e-34
34	606	64.3	258	2	US-08-860-Sequence 13, Applicat	5.04e-34
35	605	64.2	113	1	US-08-470-Sequence 46, Applicat	5.95e-34
36	605	64.2	113	1	US-08-667-Sequence 46, Applicat	5.95e-34
37	605	64.2	113	4	PCT-US93-1-Sequence 46, Applicat	5.95e-34
38	605	64.2	113	2	US-08-940-Sequence 46, Applicat	5.95e-34
39	605	64.2	113	1	US-08-467-Sequence 46, Applicat	5.95e-34
40	605	64.2	553	2	US-08-263-Sequence 9, Applicat	5.95e-34
41	605	64.2	553	2	US-08-263-Sequence 7, Applicat	7.03e-34
42	604	64.1	113	4	PCT-US93-0-Sequence 4, Applicat	8.27e-34
43	603	63.9	132	2	US-08-477-Sequence 91, Applicat	8.27e-34
44	603	63.9	132	1	US-08-477-Sequence 91, Applicat	8.27e-34
45	603	63.9	132	2	US-08-472-Sequence 91, Applicat	8.27e-34

ALIGNMENTS

RESULT 1
ID US-08-353-400-37 STANDARD: PRT: 239 AA.

AC xxxxxx

DT

XX

DE

Sequence 37, Application US/08353400

CC

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE 239 AA: 26333 MW, 321663 CN;

Query Match 86.7%; Score 818; DB 1; Length 239;
Best local similarity 84.8%; Pred. No. 2.71e-49;

Matches 112; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Db 1 MDSQAQVLLILLMWSGTGDIVYMSQSPSLAVSAGEKYTMCKSSQSLNSTRKNYIA 60

1 MDSQAQVLLILLMWSGTGDIVYMSQSPSLAVSAGEKYTMCKSSQSLNSTRKNYIA 60

1 MDSQAQVLLILLMWSGTGDIVYMSQSPSLAVSAGEKYTMCKSSQSLNSTRKNYIA 60

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```
XX XX      Sequence 9, Application PC/TUS9311611  
DT XX      DE  
CC CC      Sequence 9, Application PC/TUS9311611  
CC CC      GENERAL INFORMATION:  
CC CC      APPLICANT: Co Man Sung  
CC CC      APPLICANT: Landolfi, Nicholas F.  
CC CC      TITLE OF INVENTION: Humanized Antibodies Reactive with CD18  
CC CC      NUMBER OF SEQUENCES: 11  
CC CC      CORRESPONDENCE ADDRESS:  
CC CC      ADDRESSEE: Townsend and Townsend Kourie and Crew  
CC CC      STREET: One Market Plaza, Steuart Tower, Suite 2000  
CC CC      CITY: San Francisco  
CC CC      STATE: California  
CC CC      COUNTRY: USA  
CC CC      ZIP: 94105  
CC CC      COMPUTER READABLE FORM:  
CC CC      MEDIUM TYPE: Floppy disk  
CC CC      OPERATING SYSTEM: IBM PC compatible  
CC CC      SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CC      CURRENT APPLICATION DATA:  
CC CC      APPLICATION NUMBER: PCT/US93/11611  
CC CC      FILING DATE: 30-NOV-1993  
CC CC      CLASSIFICATION:  
CC CC      PRIOR APPLICATION DATA:  
CC CC      APPLICATION NUMBER: US 07/983,949  
CC CC      FILING DATE: 01-DEC-1992  
CC CC      ATTORNEY/AGENT INFORMATION:  
CC CC      NAME: Smith, William M.  
CC CC      REGISTRATION NUMBER: 30,223  
CC CC      REFERENCE/DOCKET NUMBER: 11823-45  
CC CC      TELECOMMUNICATION INFORMATION:  
CC CC      TELEPHONE: 415-326-2400  
CC CC      TELEFAX: 415-326-2422  
CC CC      INFORMATION FOR SEQ ID NO: 9:  
CC CC      SEQUENCE CHARACTERISTICS:  
CC CC      LENGTH: 133 amino acids  
CC CC      TYPE: amino acid  
CC CC      TOPOLOGY: linear  
CC CC      MOLECULE TYPE: protein  
SQ SQ      SEQUENCE 133 AA; 14866 MW; 109104 CN;  
  
Query Match          74.0%; Score 698; DB 4; Length 133;  
Best Local Similarity 71.4% Pred.No.1.25e+40;  
Matches    95; Conservative   18; Mismatches 19; Indels 1; Gaps 1;
```

Dd

Db

Dy

Dz

Eg

Ff

Gg

Hh

Ii

Jj

Kk

Ll

Mm

Nn

Oo

Pp

Qq

Rr

Ss

Tt

Vv

Ww

Xx

```
CC GENERAL INFORMATION:
CC APPLICANT: Koentgen, Frank
CC APPLICANT: Suess, Gabriele M.
CC APPLICANT: Tarlinton, David M.
CC APPLICANT: Treutlein, Herbert R.
CC TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
CC TITLE OF INVENTION: PRODUCING SAME
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
CC STREET: 400 Garden City Plaza
CC CITY: Garden City
CC STATE: New York
CC COUNTRY: United States of America
CC ZIP: 11530
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/828,741B
CC FILING DATE: 26-MAR-1997
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Digiglio, Frank S.
CC REGISTRATION NUMBER: 31,346
CC REFERENCE/DOCKET NUMBER: 10591
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (516) 742-4343
CC TELEFAX: (516) 742-4366
CC TELEX: 230 901 SANS UR
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 495 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 495 AA; 51894 MW; 1309376 CN;
QY Query Match 73.9%; Score 697; DB 3; Length 495;
Best Local Similarity 85.6%; Pred. No. 1,47e-40;
Matches 101; Conservative 6; Mismatches 10; Indels 1; Gaps 1.
Db 365 SGGGGDIYMTPSPDLSLAVSLGERATINCKSSQVLYSSNSKNYLAWYOQRPGPPKLLIY 424
OY 16 SGTGCGDIYLTQSPDSLAVSLGERATISCKSSQSLSLNRTRENTLAWYQKRGQPKLLIY 75
Db 425 WASTRESSVPDRPFGSGSGSDTFITITISSLAEDVAIVYYCOQYSTPYSEGCGRLEK 482
OY 76 WASTRESSVPDRPFGSGSGSDTFITITISSLAEDVAIVYYCTQSYNL-YTFGQGRKEIK 132
RESULT 8 STANDARD; PRT: 155 AA.
ID US-08-828-741B-11
XX xxxxxx
XX
XX
XX Sequence 11, Application US/08828741B
DE Sequence 11, Application US/08828741B
XX
XX Patent No. 6043069
CC GENERAL INFORMATION:
CC APPLICANT: Koentgen, Frank
CC APPLICANT: Suess, Gabriele M.
CC APPLICANT: Tarlinton, David M.
CC APPLICANT: Treutlein, Herbert R.
CC TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
CC TITLE OF INVENTION: PRODUCING SAME
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
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CC ADDRESS: SCULLY, SCOTT MURPHY & PRESSER
CC STREET: 400 Garden City Plaza
CC City: Garden City
CC STATE: New York
CC COUNTRY: United States of America
CC ZIP: 11530
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/828,741B
CC FILING DATE: 26-MAR-1997
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: DIGiglio, Frank S.
CC REGISTRATION NUMBER: 31,346
CC REFERENCE/DOCKET NUMBER: 10591
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (516) 742-4343
CC TELEFAX: (516) 742-4366
CC TELEX: 230 901 SANS DR
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 155 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC
SQ SEQUENCE 155 AA; 16932 MW; 135999 CN;
Query Match 72.7%; Score 686; DB 3; Length 155;
Best Local Similarity 86.7%; Pred. No. 9,10e-40;
Matches 98; Conservative 6; Mismatches 8; Indels 1; Gaps 1
Db 30 DIVVTQSPDLSAVSIGEATINCSSQSVLSSSKNYLAWYQOKPGQPKLLIYMASTR 89
QY 21 DIVLTQSPDSLAVSIGEATINCSSQSVLSSSKNYLAWYQOKPGQPKLLIYMASTR 80
Db 90 ESGVPRFSGSGGTDFLTLLTSSLAQAEADVAVYCYQYYSPFYSFGQGTLEIK 142
QY 81 ESGVPRFSGSGGTDFLTLLTSSLAQAEADVAVYCYQYYSPFYSFGQGTLEIK 132
RESULT 9 STANDARD; PRT; 342 AA.
ID US-08-828-741B-6
XX AC xxxxxx
XX DT
XX
XX
DE Sequence 6, Application US/08828741B
XX DE
XX Patent No. 6043069
CC GENERAL INFORMATION:
CC APPLICANT: Koentgen, Frank
CC APPLICANT: Suess, Gabriele M.
CC APPLICANT: Tarlington, David M.
CC APPLICANT: Trentlein, Herbert R.
CC TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
CC NUMBER OF SEQUENCES: 14
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
CC STREET: 400 Garden City Plaza
CC City: Garden City
CC STATE: New York
CC COUNTRY: United States of America
CC ZIP: 11530
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible

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CC      OPERATING SYSTEM:  PC-DOS/MS-DOS
CC      SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER:  US/08/828,741B
CC      FILING DATE:  26-MAR-1997
CC      CLASSIFICATION:  435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME:  Digiglio, Frank S.
CC      REGISTRATION NUMBER:  31,346
CC      REFERENCE/DOCKET NUMBER:  10591
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE:  (516) 742-4343
CC      TELEFAX:  (516) 742-4366
CC      TELEX:  230 901 SANS UR
CC      INFORMATION FOR SEQ ID NO:  6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 342 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE  342 AA; 36371 MW; 598487 CN;
SQ
Query Match          72.7%  Score 686; DB 3; Length 342;
Best Local Similarity 86.7%  Pred. 9,10e-40;
Matches  96; Conservative  6; Mismatches  8; Indels  3; Gaps  1;

Db      30 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNLAWYQKRGQPKLLTQVASTR 89
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      21 DIVLQSPDSLAVSLGERATISCKSSQSLNSRTRNTLAWYQKRGQPKLLITVASTR 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db      90 ESVGVDRRSGSGGTDFLLTITSSLAQEDVAVYYCCQYISTPYSGCGTKLEIK 141
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      81 ESVGVDRRSGSGGTDFLLTITSSLAQEDVAVYYCTOSYNL-YTFGCGTKRVEIK 132
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT  10
ID      US-08-360-125-6          STANDARD;          PRT;          114 AA.
XX      AC          xxxxxx
XX      DT
XX      DE          Sequence 6, Application US/08360125
XX      SE          Patent No. 5767246
XX      AC          GENERAL INFORMATION:
CC      APPLICANT:  Saiko HOSOKAWA
CC      APPLICANT:  Toshiaki TAGAWA
CC      APPLICANT:  Yoko HIRAKAWA
CC      APPLICANT:  NO. 5767246Ihiko ITO
CC      APPLICANT:  Kazuhiko NAGAIKE
CC      TITLE OF INVENTION:  Human Monoclonal Antibody
CC      TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
CC      NUMBER OF INVENTION:  Cell Membrane
CC      NUMBER OF SEQUENCES:  42
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE:  Wenderoth, Lind & Ponack
CC      STREET:  805 Fifteenth Street, N.W., #700
CC      CITY:  Washington
CC      STATE:  D.C.
CC      COUNTRY:  U.S.A.
CC      ZIP:  20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
CC      COMPUTER:  IBM Compatible
CC      OPERATING SYSTEM:  MS-DOS
CC      SOFTWARE:  Wordperfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER:  US/08/360,125
CC      FILING DATE:
CC      CLASSIFICATION:  424
CC      PRIOR APPLICATION DATA:

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CC APPLICATION NUMBER: 07/905,534
CC FILING DATE: June 29, 1992
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Warren M. Cheek, Jr.
CC REGISTRATION NUMBER: 33,367
CC REFERENCE/DOCKET NUMBER:
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-371-8830
CC TELEFAX:
CC
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 114 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC HYPOTHEetical:
CC ANTI-SENSE:
CC FRAGMENT TYPE:
CC ORIGINAL SOURCE:
CC ORGANISM:
CC STRAIN:
CC INDIVIDUAL ISOLATE:
CC DEVELOPMENTAL STAGE:
CC HAPLOTYPE:
CC TISSUE TYPE:
CC CELL TYPE: Hybridoma producing human
CC CELL TYPE: antibody GAH
CC CELL LINE:
CC ORGANELLE:
CC IMMEDIATE SOURCE:
CC LIBRARY:
CC CLONE:
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT:
CC MAP POSITION:
CC UNITS:
CC FEATURE:
CC NAME/KEY:
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION:
CC PUBLICATION INFORMATION:
CC AUTHORS:
CC TITLE:
CC JOURNAL:
CC VOLUME:
CC ISSUE:
CC PAGES:
CC DATE:
CC DOCUMENT NUMBER:
CC FILING DATE:
CC PUBLICATION DATE:
CC RELEVANT RESIDUES IN SEQ ID NO:
CC SEQUENCE 114 AA; 12731 MW; 76848 CN;
CC
CC Query Match 71.7%; Score 676; DB 1; Length 114;
CC Best Local Similarity 85.8%; Pred. No. 4,77e-39;
CC Matches 97; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
CC
Db 1 DIVMOSPSDLAVSLGERATINCASSQSQSVLYNSNNKRYLAWYQOKPCQPPKLLIYMASTR 60
QY 21 DIVLQSPDLSLAVSLGERATISCKSSQSLNSRTRENYLAWYQOKPCQPPKLLIYMASTR 80
61 ESGVDFRSGSGSGTDFLTITSSLQAEVAVYYCCQXYSTPWRGSGTKVEIK 113
81 ESGVDFRSGSGSGTDFLTITSSLQAEVAVYYCTQSYINL-YTFGSGTKVEIK 132

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ID US-09-017-628-6 STANDARD: PRT: 114 AA.
 XX xxxxxx
 AC
 DE Sequence 6, Application US/09017628
 CC Sequence 6, Application US/09017628
 CC Patent No. 5990287
 CC GENERAL INFORMATION:
 CC APPLICANT: HOSOKAWA, Saito
 CC APPLICANT: TAGAWA, Toshiaki
 CC APPLICANT: HIRAKAWA, Yoko
 CC APPLICANT: ITO, No. 5990287, Ithiko
 CC APPLICANT: NAGAIKE, Kazuhiko
 CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
 CC TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
 CC FILE REFERENCE: 177/527361K
 CC CURRENT APPLICATION NUMBER: US/09/017, 628
 CC CURRENT FILING DATE: 1998-02-02
 CC EARLIER APPLICATION NUMBER: 08/360, 125
 CC EARLIER FILING DATE: 1994-12-20
 CC NUMBER OF SEQ ID NOS: 42
 CC SOFTWARE: PatentIn Ver. 2.0
 CC SEQ ID NO 6
 CC LENGTH: 114
 CC TYPE: PRT
 CC ORGANISM: Unknown
 CC FEATURE:
 CC OTHER INFORMATION: Hybridoma producing human antibody GAH
 SO SEQUENCE 114 AA: 12731 MW: 76848 CN:

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Query March          71.7%; Score 676; DB 2; Length 114;
Best Local Similarity 85.88; Pred.No.4,77e-39;
Matches 97; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Db      1 DIVATGSPDSLAVLSLEERATINCKSSQSVLYVNSNNKRIAWYOOKPGOPPKLLYYMSTR 60
        |||:|||||||:|||||||:|||||||: : |||||:|||||||:|||||
Oy      21 DIVLTGSPDSLAVSLGERATISCKRSSQSILNRTENTLANTYOKRPGOPPKLLYYMSTR 80
        |||:|||||||:|||||||:|||||||: : |||||:|||||||:|||||

Oy      61 EGGVPDRFFSGSGSGTDFTLTISLSQAEDVAHYVCQQYISTPWTFGQGTYKEIK 13
        |||:|||||||:|||||||:|||||||: : |||||:|||||||:|||||
        81 EGGVPDRFSGSGSGTDFTLTISLSQAEDVAHYVCQTGYNL-VTGGQGKYVEIK 32

RESULT   12
ID US-08-450-578-6 STANDARD; PRT; 114 AA.
AC xxxxxx
XX
XX
XX
XX
DE Sequence 6, Application US/08450578
XX
CC Sequence 6, Application US/08450578
CC Patent No. 5837845
CC GENERAL INFORMATION:
CC APPLICANT: Saiko HOSOKAWA
CC APPLICANT: Toshitaki TAGAMA
CC APPLICANT: Yoko HIIRAKAWA
CC APPLICANT: No. 5837845Hiko ITO
CC APPLICANT: Kazuhito NGAIKE
CC TITLE OF INVENTION: Human Monoclonal Antibody
CC TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
CC TITLE OF INVENTION: Cell Membrane
CC NUMBER OF SEQUENCES: 42
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Wenderoth, Lind & Ponack
CC STREET: 805 Fifteenth Street, N.W., #700
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: U.S.A.

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CC      ZIP: 20005
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: MS-DOS
CC      SOFTWARE: Wordperfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/450, 578
CC      FILING DATE: May 25, 1995
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/360, 125
CC      FILING DATE: December 20, 1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/905, 534
CC      FILING DATE: June 29, 1992
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Warren M. Cheek, Jr.
CC      REGISTRATION NUMBER: 33,367
CC      REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-371-8850
CC      TELEFAX:
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 114 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      HYPOTHETICAL:
CC      ANTI-SENSE:
CC      FRAGMENT TYPE:
CC      ORIGINAL SOURCE:
CC      ORGANISM:
CC      STRAIN:
CC      INDIVIDUAL ISOLATE:
CC      DEVELOPMENTAL STAGE:
CC      HAPLOTYPE:
CC      TISSUE TYPE:
CC      CELL TYPE: Hybridoma producing human
CC      CELL LINE: antibody G4H
CC      ORGANELLE:
CC      IMMEDIATE SOURCE:
CC      LIBRARY:
CC      CLONE:
CC      POSITION IN GENOME:
CC      CHROMOSOME/SEGMENT:
CC      MAP POSITION:
CC      UNITS:
CC      FEATURE:
CC      NAME/KEY:
CC      LOCATION:
CC      IDENTIFICATION METHOD:
CC      OTHER INFORMATION:
CC      PUBLICATION INFORMATION:
CC      AUTHORS:
CC      TITLE:
CC      JOURNAL:
CC      VOLUME:
CC      ISSUE:
CC      PAGES:
CC      DATE:
CC      DOCUMENT NUMBER:
CC      FILING DATE:
CC      PUBLICATION DATE:
CC      RELEVANT RESIDUES IN SEQ ID NO:
CC      SEQUENCE 114 AA; 12731 MW; 76848 CN;
CC
CC      Query Match 71.7%; SCORE 676; DB 2; Length 114;
CC      Best Local Similarity 83.8%; Pred. No. 4.77e-39;

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Matches      97;  Conservative      6;  Mismatches      9;  Indels      1;  Gaps      1;

Db      1  DIVTQSPDLSAVSLGERATINCKSSQSVLYNSNNKYYIAWYQKPGQPKLLIYWASTR 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      21  DIVLTQSPDLSAVSLGERATISCKSSQSVLSLNSRTRENYIAWYQKPGQPKLLIYWASTR 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db      61  ESGVPDRPSGSGSTDFLTITSSLOAEDVAVVYCCQYYSPTWFGGQTVETK 113
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      81  ESGVPDRPSGSGSTDFLTITSSLOAEDVAVVYCTQSYNL-YTFGGQTVETK 132

RESULT      13
ID      US-09-014-880-6      STANDARD;      PRT;      114 AA.
AC      xxxxxx
DT
XX
XX
Sequence 6, Application US/09014880
CC
CC      Sequence 6, Application US/09014880
CC      Patent No. 5990297
CC      GENERAL INFORMATION:
CC      APPLICANT: Saiko HOSOKAWA et al.
CC      TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
CC      TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
CC      NUMBER OF SEQUENCES: 42
CC      CORRESPONDENCE ADDRESSES:
CC      ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
CC      STREET: 2033 K Street, N.W., #800
CC      CITY: Washington
CC      STATE: D.C.
CC      COUNTRY: U.S.A.
CC      ZIP: 20006
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: MS-DOS
CC      SOFTWARE: Wordperfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/09/014,880
CC      FILING DATE: January 28, 1998
CC      CLASSIFICATION: 536
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/450,578
CC      FILING DATE: May 25, 1995
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/360,125
CC      FILING DATE: December 20, 1994
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/905,534
CC      FILING DATE: June 29, 1992
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Warren M. Cheek, Jr.
CC      REGISTRATION NUMBER: 33,367
CC      REFERENCE/DOCKET NUMBER:
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-721-8200
CC      TELEFAX: 202-721-8250
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 6:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 114 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      ORIGINAL SOURCE:
CC      CELL TYPE: Hybridoma producing human
CC      CELL TYPE: antibody GAH
CC      SEQUENCE      114 AA, 12731 MW, 76848 CN;
50
Query Match      71.7%, Score 676; DB 2; Length 114;

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Best Local Similarity 85.8%; Pred. No. 4.77e-39;
Matches 97; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Db 1 DIVMTOSPDLSAVSLGERATINCKSSOSLVNSNKKIYLAQQKPGQPPKLLIYMASTR 60
OY 21 DIVLTPSPDLSAVSLGERATISCKSSOSLNSRTRENTLAWYQKPGQPPKLLIYMASTR 80
Db 61 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCCQYSTPRTFGGTVEIK 113
OY 81 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCTQSYNL-YTFGGGTVEIK 132

RESULT 14
ID PCT-US93-08435-8 STANDARD: PRT: 113 AA.
XX xxxxxx

Sequence 8, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 113 AA; 12523 MW; 75327 CN;

Query Match 71.6%; Score 675; DB 4; Length 113;
Best Local Similarity 87.6%; Pred. No. 5.63e-39;
Matches 99; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

Db 1 DIVMTOSPDLSAVSLGERATINCKSSOSLVNSNKKIYLAQQKPGQPPKLLIYMASTR 60
OY 21 DIVLTPSPDLSAVSLGERATISCKSSOSLNSRTRENTLAWYQKPGQPPKLLIYMASTR 80

Db 61 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCCQYSTPRTFGGTVEIK 113
OY 81 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCTQSYNL-YTFGGGTVEIK 132

RESULT 15
ID PCT-US93-08435-6 STANDARD: PRT: 113 AA.
XX xxxxxx

Sequence 6, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 113 AA; 12513 MW; 75376 CN;

Query Match 70.8%; Score 668; DB 4; Length 113;
Best Local Similarity 86.7%; Pred. No. 1.79e-38;
Matches 98; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Db 1 DIVMTOSPDLSAVSLGERATINCKSSOSLVNSNKKIYLAQQKPGQPPKLLIYMASTR 60
OY 21 DIVLTPSPDLSAVSLGERATISCKSSOSLNSRTRENTLAWYQKPGQPPKLLIYMASTR 80
Db 61 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCCQYSTPRTFGGTVEIK 113
OY 81 ESGVDPDRFSSGSGTDFTLTISLSQAEDVAVYYCTQSYNL-YTFGGGTVEIK 132

Search completed: Mon Aug 7 19:05:27 2000
Job time : 10 secs.

